



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 116910

TO: Karen A Lacourciere

Location: rem/2d15/2c18

Art Unit: 1635

March 22, 2004

Case Serial Number: 09/260624

From: P. Sheppard

Location: Remsen Building

Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

STIC-Biotech/ChemLib

116910

From: Fredman, Jeffrey
Sent: Wednesday, March 17, 2004 9:53 AM
To: STIC-Biotech/ChemLib
Cc: Lacourciere, Karen
Subject: FW: Rush sequence search approval 09/260,624

RECEIVED
MAR 17 2004
STIC

This was already submitted, but if possible please rush.

I Approve.

Jeff Fredman

-----Original Message-----

From: Lacourciere, Karen
Sent: Monday, March 15, 2004 11:13 AM
To: Fredman, Jeffrey
Subject: Rush sequence search approval 09/260,624

Hi Jeff-

Could you approve a RUSH for this search? The case is about to hit the 4 month date, Jhn wants it done ASAP. The search by the prior Examiner is not in the case and the claims have been broadened that new art will probably need to be applied.

Thank you!
Karen

Please search SEQ ID NO:1 and 2 in the commercial databases and in pre-grant pubs.
Thank-you

Karen A. Lacourciere Ph.D.

Remsen 2D15 GAU 1635
(571) 272-0759
mailbox Remsen 2C18

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 3/22/04
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 20:50:14 ; Search time 2409 Seconds
(without alignments)
185.941 Million cell updates/sec

Title: US-09-260-624A-2
Perfect score: 15
Sequence: 1 egtatgacagatctg 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estlin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estcom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pin:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_man:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_pig:*
 - 27: em_gss_vrl:*
 - 28: gb_gss1:*
 - 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15	100.0	220	13	BQ226183
C 2	15	100.0	226	10	BG001759
C 3	15	100.0	230	14	T19802
C 4	15	100.0	239	10	BF086893

C 5	15	100.0	246	10	BF085986
C 6	15	100.0	342	29	CG566143
C 7	15	100.0	351	13	BQ316480
C 8	15	100.0	353	13	BQ316481
C 9	15	100.0	413	12	BG797804
C 10	15	100.0	414	12	BM796675
C 11	15	100.0	423	14	CA560591
C 12	15	100.0	423	29	CG641066
C 13	15	100.0	424	29	CG616284
C 14	15	100.0	433	14	N72527
C 15	15	100.0	436	9	AA474058
C 16	15	100.0	436	29	CG583628
C 17	15	100.0	446	29	CG594299
C 18	15	100.0	446	29	CG801951
C 19	15	100.0	453	29	CG591152
C 20	15	100.0	455	29	CG604679
C 21	15	100.0	477	29	CG568851
C 22	15	100.0	480	29	CG597990
C 23	15	100.0	487	14	CF139164
C 24	15	100.0	490	14	CB220639
C 25	15	100.0	511	29	CG836459
C 26	15	100.0	595	13	BG898500
C 27	15	100.0	617	14	CF951196
C 28	15	100.0	619	14	CA531310
C 29	15	100.0	640	10	BB614123
C 30	15	100.0	651	12	BG480368
C 31	15	100.0	651	29	CG533806
C 32	15	100.0	661	10	BE779265
C 33	15	100.0	661	13	BY744039
C 34	15	100.0	667	10	BF468350
C 35	15	100.0	673	12	BM011814
C 36	15	100.0	673	13	BY744015
C 37	15	100.0	677	29	AG131725
C 38	15	100.0	682	10	BB643278
C 39	15	100.0	683	10	BF132395
C 40	15	100.0	688	12	BG325079
C 41	15	100.0	693	13	BY734800
C 42	15	100.0	699	10	BF161108
C 43	15	100.0	701	10	BE312219
C 44	15	100.0	706	10	BF133593
C 45	15	100.0	708	12	BI826961

ALIGNMENTS

RESULT 1
BQ226183/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BQ226183
AGENCOURT_7572631 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6044738
5', mRNA sequence.
BQ226183
BQ226183.1 GI:20407583
EST.
Homo sapiens (human)

220 bp
mRNA
linear
EST 02-MAY-2002

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC <http://mgc.nci.nih.gov/>.
1 (bases 1 to 220)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ARCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13287 row: n column: 03
High quality sequence start: 25

High quality sequence stop: 219.

FEATURES

Location/Qualifiers
1..220
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6044738"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dn primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 220;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
|||||
Db 44 CGTATGACAGATCTG 30

RESULT 2

BG001759/c
LOCUS 226 bp mRNA linear EST 24-JAN-2001
DEFINITION CM3-GN0049-151100-359-F10 GN0049 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG001759
VERSION BG001759.1 GI:12440410
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 226)
AUTHORS Dias Neto, E., Garcia Correa, R., Vertovski-Almeida, S., Briones, M.R., Nagai, M.A., de Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.P., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Sucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202633
PubMed 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-GN0049-151100-359-F10&t3=2000-11-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 36
High quality sequence stop: 226.
Location/Qualifiers
1..226
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0049"
/note="Organ: placenta normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning

FEATURES

Source
1..226
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0049"
/note="Organ: placenta normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning

ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
|||||
Db 219 CGTATGACAGATCTG 205

RESULT 3

T19802
LOCUS 230 bp mRNA linear EST 28-NOV-1994
DEFINITION B555F Heart Homo sapiens cDNA clone B555 similar to RecA-like protein HeRad51, mRNA sequence.

ACCESSION T19802
VERSION T19802.1 GI:597547
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 230)
AUTHORS Liaw, C.C., Hwang, D.M., Fung, Y.W., Laurensen, C., Cukerman, E., Tsui, S. and Lee, C.Y.
TITLE A catalogue of genes in the cardiovascular system as identified by expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91, 10645-10649 (1994)
MEDLINE 95024171
PubMed 7938007
COMMENT Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 61779750995
Email: cilew@rics.bwh.harvard.edu
Seq primer: GGTGGCAGCACTCTGGAGCC.

FEATURES

Source
1..230
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="B555"
/lab_host="E.coli Y1090"
/clone_lib="Heart"
/note="Vector: Lambda gt11; Site 1: EcoRI; Site 2: EcoRI"

ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
|||||
Db 36 CGTATGACAGATCTG 50

RESULT 4

BF086893/c
LOCUS 239 bp mRNA linear EST 19-OCT-2000
DEFINITION CM3-GN0092-160900-353-c03 GN0092 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF086893
VERSION BF086893.1 GI:10892603
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 239)
AUTHORS Liaw, C.C., Hwang, D.M., Fung, Y.W., Laurensen, C., Cukerman, E., Tsui, S. and Lee, C.Y.
TITLE A catalogue of genes in the cardiovascular system as identified by expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91, 10645-10649 (1994)
MEDLINE 95024171
PubMed 7938007
COMMENT Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 61779750995
Email: cilew@rics.bwh.harvard.edu
Seq primer: GGTGGCAGCACTCTGGAGCC.

products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

FEATURES

source

Location/Qualifiers
1..342
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129SV/Ev"
/db_xref="taxon:10090"
/clone="OST191539"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129SV/Ev"

ORIGIN

Query Match 100.0%; Score 15; DB 29; Length 342;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15

Db 324 CGTATGACAGATCTG 310

RESULT 7

BQ316480/c
LOCUS BQ316480 351 bp mRNA linear EST 17-MAY-2002
DEFINITION PM4-CT0331-291199-001-A06 CT0331 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ316480
VERSION BQ316480.1 GI:20922249
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 351)

AUTHORS

Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R., Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F., Goldman G.H., Carvalho A.F., Matsukuma A., Baia G.S., Simpson D.H., Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and Simpson A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
PUBMED
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM4&t2=PM4-CT0331-291199-001-A06&t3=1999-11-29&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 351.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM4&t2=PM4-CT0331-291199-001-A06&t3=1999-11-29&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 351.

FEATURES

source

Location/Qualifiers
1..351
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0331"

/notes="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 353;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15

Db 152 CGTATGACAGATCTG 138

stringency conditions."

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 351;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15

Db 150 CGTATGACAGATCTG 136

RESULT 8

BQ316481/c

LOCUS BQ316481 353 bp mRNA linear EST 17-MAY-2002

DEFINITION PM4-CT0331-291199-001-A11 CT0331 Homo sapiens cDNA, mRNA sequence.

ACCESSION BQ316481

VERSION BQ316481.1 GI:20922250

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 353)

AUTHORS Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R., Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F., Goldman G.H., Carvalho A.F., Matsukuma A., Baia G.S., Simpson D.H., Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and Simpson A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM4&t2=PM4-CT0331-291199-001-A11&t3=1999-11-29&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 353.

Location/Qualifiers

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/organism="Homo sapiens"

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/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="CT0331"

/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low

stringency conditions."

```

RESULT 9
BG797804
LOCUS
DEFINITION
ic07a08.x1 Kaestner ngn3 - Mus musculus cDNA 3', similar to
SW:R51_RABIT_077507 DNA REPAIR PROTEIN RAD51 HOMOLOG 1. ;, mRNA
sequence.
ACCESSION
BG797804
VERSION
BG797804.1 GI:14144906
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Melton,D., Brown,J., Kent,G., Permutt,A., Lee,C., Kaestner,K.,
Lenishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Page,D., Wylie,T., Martin,J., Blisstein,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,K., Tsagareishvili,R.,
Williams,T., Jackson,Y., and Bowers,Y.
TITLE
Endocrine Pancreas Consortium
JOURNAL
Unpublished (2000)
COMMENT
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave. Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8857
Email: dmelton@biohp.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Marie Searce
(msearce@mail.med.upenn.edu)
High quality sequence stop: 367.
FEATURES
source
1..413
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129/SV x CD1"
/db_xref="taxon:10090"
/dev_stage="p.c. 14.5"
/clone_lib="Kaestner ngn3 -"
/lab_host="E. coli-DH102S (GIBCO)"
/notes="Organ: pancreas; Vector: pSPORT2 (GIBCO); Site_1:
Not 1; Site_2: Sal I; The library was prepared by
Catherine S. Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000). The cDNA's were prepared with an oligo containing a
NotI site, and SalI linkers were added to the ends. The
inserts were cut with NotI before being cloned into the
NotI-SalI sites in the vectors. This is one of two
libraries, ngn3 wt and ngn3 -/- . The ngn3 -/- library is
in pSPORT2, T7 promoter is 3'."
ORIGIN
Query Match 100.0%; Score 15; DB 12; Length 413;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCTG 15
|||||
Db 187 CGTATGACAGATCTG 201

RESULT 10
BM796675/c
LOCUS
DEFINITION
K-EST0079458 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-64-E10
5', mRNA sequence.
ACCESSION
BM796675
VERSION
BM796675.1 GI:19144907
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 414)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE
21C Frontier Korean EST Project 2001
JOURNAL
Unpublished (2002)
COMMENT
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 64 row: E column: 10
High quality sequence stop: 414.
FEATURES
source
1..414
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNU16n1-64-E10"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/lab_host="SNU-16"
/clone_lib="S22SNU16n1"
/notes="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldi, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 Cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."
ORIGIN
Query Match 100.0%; Score 15; DB 12; Length 414;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCTG 15
|||||
Db 333 CGTATGACAGATCTG 319

RESULT 11
CA560591/c
LOCUS
DEFINITION
K0274F02-5N N1A Mouse Unfertilized Egg cDNA Library (long) Mus
musculus cDNA clone N1A:K0274F02 IMAGE:30051805 5', mRNA sequence.
ACCESSION
CA560591
VERSION
CA560591.1 GI:25105246
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 423)
Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Staggs,C.A.,
Martin,P., Aiba,K., Tanaka,T. and KO,M.S.H.
TITLE
Systematic Analyses of N1A Mouse Unfertilized Egg cDNA Library
(long)
JOURNAL
Unpublished (2001)
COMMENT
Contact: Dawood B. Dudekula

```

Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@leuun.gsc.nia.nih.gov
Plate: K0274 row: F column: 02
Seq primer: M13 Reverse
High quality sequence stop: 423
POLYA-No.

FEATURES

source

Location/Qualifiers
1. .423
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:K0274F02-5N"
/db_xref="taxon:10090"
/clone="NIA:K0274F02 IMCE:30051805"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
/clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://leuun-grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen).
5'-pGATGAGTCTAGATCGGAGCGCGCCCTTTTCTTTT-3', treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. NO. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15

Db 302 CGTATGACAGATCTG 288

RESULT 12

CG641066/c

LOCUS

DEFINITION OST375200 Mus musculus 129Sv/Ev Mus musculus genomic clone
OST375200, Genomic survey sequence.

ACCESSION

CG641066

VERSION

CG641066.1 GI:37464915

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 423)

Zambrowicz B.P., Abuin A., Ramirez-Solis R., Richter L.J., Piggott J., BeltrandelRio H., Buxton E.C., Edwards J., Finch R.A., Friddle C.J., Gupta A., Hansen G., Hu Y., Huang W., Jaing C., Key B.W. Jr., Kipp P., Kohlhauff B., Ma Z.-Q., Markesich D., Payne R., Potter D.G., Qian N., Shaw J., Schrick J., Shi Z.-Z., Sparks M.J., Van Sligtenhorst I., Vogel P., Walke W., Xu N., Zhu Q., Person C. and Sands A.T.

TITLE

JOURNAL

COMMENT

Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank

FEATURES

source

Location/Qualifiers

1. .423

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST375200"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match

Best Local Similarity

Matches

15; Conservative

0; Mismatches

0; Indels

0; Gaps

QY 1 CGTATGACAGATCTG 15

Db 416 CGTATGACAGATCTG 402

RESULT 13

CG616284/c

LOCUS

DEFINITION

CGS108246 Mus musculus 129Sv/Ev Mus musculus genomic clone

OST308246, genomic survey sequence.

ACCESSION

CG616284

VERSION

CG616284.1 GI:37440133

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 424)

Zambrowicz B.P., Abuin A., Ramirez-Solis R., Richter L.J., Piggott J., BeltrandelRio H., Buxton E.C., Edwards J., Finch R.A., Friddle C.J., Gupta A., Hansen G., Hu Y., Huang W., Jaing C., Key B.W. Jr., Kipp P., Kohlhauff B., Ma Z.-Q., Markesich D., Payne R., Potter D.G., Qian N., Shaw J., Schrick J., Shi Z.-Z., Sparks M.J., Van Sligtenhorst I., Vogel P., Walke W., Xu N., Zhu Q., Person C. and Sands A.T.

TITLE

JOURNAL

COMMENT

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. .424

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST308246"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match

Best Local Similarity

Matches

15; Conservative

0; Mismatches

0; Indels

0; Gaps

QY 1 CGTATGACAGATCTG 15

Db 416 CGTATGACAGATCTG 402


```

Query Match      100.0%; Score 15; DB 29; Length 424;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 417 CGTATGACAGATCTG 403

RESULT 14
N72527/c
LOCUS
DEFINITION
Yv43h12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
(HUMAN); contains element MBR22 repetitive element ; , mRNA sequence.
ACCESSION N72527
VERSION N72527.1 GI:1229631
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 433)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisan,S.B., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LInL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 355 Std Error: 0.00
Seq primer: reverse ET
High quality sequence stop: 384.
Location/Qualifiers
1. 433
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3794789"
/db_xref="taxon:9606"
/clone="IMAGE:245543"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5', AACGCGAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

Query Match      100.0%; Score 15; DB 14; Length 433;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 67 CGTATGACAGATCTG 53

Query Match      100.0%; Score 15; DB 9; Length 436;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 243 CGTATGACAGATCTG 229

RESULT 15
AA474058/c
LOCUS
DEFINITION
v554cl1.r1 Beddington mouse embryonic region Mus musculus CDNA
clone IMAGE:821972 5', similar to gb:DI4134 DNA REPAIR PROTEIN RAD51
HOMOLOG (HUMAN); gb:DI3803 Mouse mRNA for RECA-like protein
MmrRad51, complete cds (MOUSE); , mRNA sequence.
ACCESSION AA474058
VERSION AA474058.1 GI:2202285
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 436)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Treising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LInL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:490252
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 229.
Location/Qualifiers
1. 436
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6 x DBA"
/db_xref="taxon:10090"
/clone="IMAGE:821972"
/sex="pooled"
/tissue_type="embryo"
/dev_stage="7.5dpc"
/lab_host="DH12S"
/clone_lib="Beddington mouse embryonic region"
/note="Organ: whole embryo; Vector: pCMV-SPORT; Site_1:
SalI; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Gastrulating embryos were collected at 7.5dpc
from C57BL6 x DBA matings, excluding embryos that had
developed head folds and all extraembryonic tissues.
Average insert size: 1.3 kb (range: 0.5 - 3.0 kb).
Referenced in Development 121, 2479-2489 (1995)"

Query Match      100.0%; Score 15; DB 14; Length 433;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 67 CGTATGACAGATCTG 53

Query Match      100.0%; Score 15; DB 14; Length 433;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 67 CGTATGACAGATCTG 53

Search completed: March 21, 2004, 23:22:49
Job time : 2423 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 20:50:14 ; Search time 2409 Seconds
(without alignments)
185.941 Million cell updates/sec

Title: US-09-260-624A-1

Perfect score: 15

Sequence: 1 ggcttcaataatcc 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pig:*

27: em_gss_vil:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	269	AQ463196	AQ463196 HS 5199 B
2	15	100.0	328	BU221983	BU221983 603756554
3	15	100.0	396	CA531739	CA531739 C0324803
4	15	100.0	404	BY227299	BY227299 BY227299

C 5	15	100.0	414	12	BM796675
C 6	15	100.0	423	14	CA560591
C 7	15	100.0	423	29	CG641066
C 8	15	100.0	427	13	EX494877
C 9	15	100.0	436	9	AA474058
C 10	15	100.0	437	12	BG798213
C 11	15	100.0	446	29	CG594299
C 12	15	100.0	446	29	CG601951
C 13	15	100.0	449	13	BY030621
C 14	15	100.0	453	29	CG591152
C 15	15	100.0	454	13	EX475529
C 16	15	100.0	455	29	CG604679
C 17	15	100.0	467	13	BY030738
C 18	15	100.0	471	13	BY030677
C 19	15	100.0	479	14	CA557006
C 20	15	100.0	480	29	CG597990
C 21	15	100.0	511	12	BI067879
C 22	15	100.0	511	29	CG626459
C 23	15	100.0	512	13	BU252761
C 24	15	100.0	533	13	BX260018
C 25	15	100.0	533	14	CD562647
C 26	15	100.0	534	12	BG085688
C 27	15	100.0	534	29	AY418335
C 28	15	100.0	534	29	AY418336
C 29	15	100.0	534	29	AY418337
C 30	15	100.0	537	10	BB858442
C 31	15	100.0	545	14	CD562793
C 32	15	100.0	547	12	BG470554
C 33	15	100.0	548	13	BU202347
C 34	15	100.0	549	10	BE280848
C 35	15	100.0	564	9	AA940166
C 36	15	100.0	584	12	BI193363
C 37	15	100.0	585	13	BU449906
C 38	15	100.0	574	9	AUL23935
C 39	15	100.0	590	14	CF899075
C 40	15	100.0	595	13	BU988500
C 41	15	100.0	615	10	BE913664
C 42	15	100.0	619	14	CA531310
C 43	15	100.0	622	12	BG474115
C 44	15	100.0	625	13	BU135803
C 45	15	100.0	626	13	BU335269

ALIGNMENTS

AQ463196 269 bp DNA linear GSS 23-APR-1999
HS 5199_B1_E10_T7A_RPCI-11 Human Male BAC Library Homo sapiens
genomic_clone Plate=775 Col=19 Row=J, genomic survey sequence.

ACCESSION AQ463196
VERSION AQ463196.1 GI:4640291
KEYWORDS GSS.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 269)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 9380589
PubMed 10449764

COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library PPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong@med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (<http://info@resgen.com>). BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 775 row: J column: 19
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 269.
 Location/Qualifiers
 1. 269
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="plate=775 Col=19 Row=J"
 /sex="male"
 /clone_lib="RPQI-11 Human Male BAC Library"
 /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methyase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

FEATURES

source

ORIGIN

Query Match 100.0%; Score 15; DB 28; Length 269;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;
 Qy 1 GGCTTCACCTAATTC 15
 |||||
 Db 173 GGCTTCACCTAATTC 187

RESULT 2

BU221983/c
 LOCUS BU221983 328 bp mRNA linear EST 25-NOV-2002
 DEFINITION 603756594F1 CSEQCHN04 Gallus gallus cdna clone CHEST668k24 5', mRNA sequence.
 ACCESSION BU221983
 VERSION BU221983.1 GI:25410698
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 1 (bases 1 to 328)
 Boardman, P.B., Sanz-Bzquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr Biol. 12 (22), 1965-1969 (2002)
 22335534
 MEDLINE 12445392
 CONTACT: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1. 328
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, HiseX"
 /db_xref="taxon:9031"
 /clone="CHEST668k24"
 /tissue_type="whole embryo"
 /dev_stage="20-21"
 /lab_host="DH10B"

FEATURES

source

/clone_lib="CSEQCHN04"
 /note="Organ: whole embryo; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; this normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;
 Qy 1 GGCTTCACCTAATTC 15
 |||||
 Db 64 GGCTTCACCTAATTC 50

RESULT 3

CAS31739/c
 LOCUS CAS31739 396 bp mRNA linear EST 18-NOV-2002
 DEFINITION C0324B03-SN NIA Mouse Undifferentiated ES Cell cDNA Library (Long) sequence.
 ACCESSION CAS31739
 VERSION CAS31739.1 GI:25061103
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Luo, A., Jaradat, S.A., Boheler, K.R. and Ko, M.S.H.
 Systematic Analyses of NIA Mouse Undifferentiated ES Cell cDNA Library (Long)
 Unpublished (2001)
 Other ESTs: C0324B03-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: C0324 row: B column: 03
 Seq primer: M13 Reverse
 High quality sequence stop: 396
 POLYA=No.

FEATURES

source

Location/Qualifiers
 1. 396
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129/Sv x 129/Sv-CP"
 /db_xref="niaEST:C0324B03-SN"
 /db_xref="taxon:10090"
 /clone="NIA:C0324B03 IMAGE:30007118"
 /tissue_type="Undifferentiated ES Cell"
 /cell_line="R1 ES cells"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse Undifferentiated ES Cell cDNA Library (Long)"
 /note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://igsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res.

11: 1553-1558 (2001). [PMID: 11544199]. Total RNAs were obtained from Dr. Kenneth R. Boheler (National Institute on Aging, USA). ES cells were cultured without feeder cells in the presence of LIF and BRL-conditioned media. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [inverted].

5'-pGACTAGTCTGATGCGAGCGCGCCCTTTTCTTTT-3' from 14.2 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Loxe-linker LL-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The pHD10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 396;
Best Local Similarity 100.0%; Pred. NO. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

Db 246 GGCTTCACTAATTC 232

RESULT 4

BY227299/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY227299 404 bp mRNA linear EST 10-DEC-2002
BY227299 RIKEN full-length enriched, erythroblast Mus musculus cDNA
clone KOC0009D13 5', mRNA sequence.

BY227299

BY227299.1 GI:26408409

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 404)

Okazaki, Y., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Nikaido, I., Furuno, M., Kasukawa, T., Adachi, C., Bono, H., Kondo, S.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojibori, T., Baldarelli, R., Hill, D. P., Bult, C.,

Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,

Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,

Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,

Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,

Sultanar, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,

Verdun, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., I.,

Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Inotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

JOURNAL

MEDLINE

PUBMED

COMMENT

Nature 420, 563-573 (2002)

22354683

12466851

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-resgsc.riken.go.jp/

URL: http://genome.gsc.riken.go.jp/

Aizawa, K., Inotani, K., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Inotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ono, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watanishi, A., Muramatsu, M. and

Hayashizaki, Y. Direct submission

Computational Analysis of Full-length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

Genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of genome exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Tissues were provided by Hiromitsu Nakauchi (Dept. of Immunology

Institute of Basic Medical Sciences University of Tsukuba 1-1-1

Tennodai, Tsukuba, Ibaraki 305-8578) whose assistance we gratefully

acknowledge. Please visit our web site

(http://genome.gsc.riken.go.jp) for further details.

Location/Qualifiers

1..404

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="KOC0009D13"

/cell_type="erythroblast"

/clone_lib="RIKEN full-length enriched, erythroblast"

/

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Query Match 100.0%; Score 15; DB 13; Length 404;
Best Local Similarity 100.0%; Pred. NO. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

Db 390 GGCTTCACTAATTC 376

RESULT 5

BM796675/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BM796675 414 bp mRNA linear EST 05-MAR-2002
K-EST0079458 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-64-B10
5', mRNA sequence.

BM796675

BM796675.1 GI:19144907

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 414)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 64 row: E column: 10
 High quality sequence stop: 414.

FEATURES

source

1. 414
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S22SNU16n1-64-E10"
 /sex="F"
 /tissue_type="Ascites"
 /cell_type="Lymphoblast-like"
 /cell_line="SNU-16"
 /lab_host="DH10B"
 /clone_lib="S22SNU16n1"
 /note="Organ: Stomach; Vector: pRT3-Pac; Site_1: EcoRI; Site_2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 Cell was established from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 414;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACATATCC 15
 |||||
 Db 123 GGCTTCACATATCC 109

RESULT 6

CA560591/c
 LOCUS
 DEFINITION K0274F02-SN NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
 musculus cDNA clone NIA:K0274F02 IMAGE:30051805 5', mRNA sequence.

ACCESSION CA560591
 VERSION
 KEYWORDS
 SOURCE EST.

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 423)

REFERENCE

Authors Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Stagg, C.A., Martin, P., Alba, K., Tanaka, T. and Ko, M.S.H.

TITLE

Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library (long)

JOURNAL

Unpublished (2001)

COMMENT

Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov

Plate: K0274 row: F column: 02

Seq primer: M13 Reverse

High quality sequence stop: 423

POLYA=No.

Location/Qualifiers

source

1. 423
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="NIA:K0274F02 IMAGE:30051805"
 /tissue_type="Unfertilized Egg"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long)"
 /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11541991]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen).
 5'-pgactagttctagatcgagcgccgcttttttttttt-3',
 treated with T4 DNA polymerase and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 423;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACATATCC 15
 |||||
 Db 92 GGCTTCACATATCC 78

RESULT 7

CG641066/c
 LOCUS
 DEFINITION OGT375200 Mus musculus 129Sv/Ev Mus musculus genomic clone
 OGT375200, genomic survey sequence.

ACCESSION CG641066
 VERSION
 KEYWORDS
 SOURCE GSS.

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 423)

REFERENCE

Authors Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Figgott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhaufl, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

COMMENT

Contact: Zambrowicz BP
 OmilBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

FEATURES

Location/Qualifiers
1..423
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129SV/Ev"
/db_xref="taxon:10090"
/clone="OST375200"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129SV/Ev"

ORIGIN

Query Match 100.0%; Score 15; DB 29; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
|||||
DB 206 GGCTTCACTAATTC 192

RESULT 8

BX494877/c

LOCUS

DEFINITION

BX494877 427 bp mRNA linear EST 04-SEP-2003
DKFZp779C0716_r1 779 (synonym: hnccl) Homo sapiens cDNA clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: MIPS

INGOLSTAEDTER Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing

consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp779C0716) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1..427

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp779C0716"

/tissue_type="liver"

/dev_stage="fetal"

/lab_host="DH10B"

/clone_lib="779 (synonym: hnccl)"

/notes="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB"

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 427;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

|||||

DB 233 GGCTTCACTAATTC 219

RESULT 9

AA474058/c

LOCUS

DEFINITION

AA474058 436 bp mRNA linear EST 18-JUN-1997
ve54c11.r1 Beddington mouse embryonic region Mus musculus cDNA
clone IMAGE:821972.5, similar to gb:D141134 DNA REPAIR PROTEIN RAD51
HOMOLOG (HUMAN); gb:D13803 Mouse mRNA for RecA-like protein
Mmrads1, complete cds (MOUSE);, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1996)

Contact: Maxra M/Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:490252

Seq primer: -28ml3 rev1 ET from Amersham

High quality sequence stop: 229.

Location/Qualifiers

1..436

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6 x DBA"

/db_xref="taxon:10090"

/clone="IMAGE:821972"

/sex="pooled"

/tissue_type="embryo"

/dev_stage="7.5dpc"

/lab_host="DH128"

/clone_lib="Beddington mouse embryonic region"

/notes="Organ: whole embryo; Vector: pCMV-SPORT; Site 1:

SalI; Site 2: NotI; Cloned unidirectionally. Primer:

Oligo dt. Gastrulating embryos were collected at 7.5dpc

from C57BL6 x DBA matings, excluding embryos that had

developed head folds and all extraembryonic tissues.

Average insert size: 1.3 kb (range: 0.5 - 3.0 kb).

Referenced in Development 121, 2479-2489 (1995)"

ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 436;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

|||||

DB 33 GGCTTCACTAATTC 19

RESULT 10

BG798213/c

LOCUS

DEFINITION

BG798213 437 bp mRNA linear EST 05-JUL-2001
ic07a08.yl Kaestner ngn3 - Mus musculus cDNA 5', similar to
SW:RAS1_RABIT 077507 DNA REPAIR PROTEIN RAD51 HOMOLOG 1.;, mRNA
sequence.

ACCESSION

VERSION

BG798213.1 GI:14162545

```

KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blustein,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisshvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTRs: sc07a08.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Marie Searce
(mscearce@mail.med.upenn.edu)
High quality sequence stop: 426.
Location/Qualifiers
1..437
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129/Sv x CD1"
/db_xref="taxon:10090"
/dev_stage="p.c. 14.5"
/lab_host="E. coli-DH12S (GIBCO)"
/clone_lib="Kaestner ngm3 -"
Note: Organ: pancreas; Vector: pSPORT2 (GIBCO); Site: 1:
Not I; Site 2: Sal I; The library was prepared by
Catherine S. Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000). The cDNA's were prepared with an oligo containing a
NotI site, and SalI linkers were added to the ends. The
inserts were cut with NotI before being cloned into the
NotI-SalI sites in the vectors. This is one of two
libraries, ngm3 wt and ngm3 -/- . The ngm3 -/- library is
in pSPORT2, T7 promoter is 3'."

ORIGIN
Query Match      100.0%; Score 15; DB 12; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
    |||||
Db 30 GGCTTCACTAATTC 16

RESULT 11
CG594299/c
LOCUS
DEFINITION
CG594299 Mus musculus 129Sv/Ev Mus musculus genomic clone
OST252329, genomic survey sequence.
ACCESSION
CG594299
VERSION
CG594299.1 GI:37405304
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,

FEATURES
source
1..446
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST252329"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Query Match      100.0%; Score 15; DB 29; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
    |||||
Db 214 GGCTTCACTAATTC 200

RESULT 12
CG601951/c
LOCUS
DEFINITION
CG601951 Mus musculus 129Sv/Ev Mus musculus genomic clone
OST274840, genomic survey sequence.
ACCESSION
CG601951
VERSION
CG601951.1 GI:37421132
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,C., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohnauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1..446
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"

FEATURES
source
1..446
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST252329"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Query Match      100.0%; Score 15; DB 29; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
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Db 214 GGCTTCACTAATTC 200

RESULT 12
CG601951/c
LOCUS
DEFINITION
CG601951 Mus musculus 129Sv/Ev Mus musculus genomic clone
OST274840, genomic survey sequence.
ACCESSION
CG601951
VERSION
CG601951.1 GI:37421132
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,C., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohnauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1..446
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"

FEATURES
source
1..446
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"

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/db_xref="taxon:10090"
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ORIGIN

Query Match      100.0%; Score 15; DB 29; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GGCCTTCACTAATTC 15
        |||
Db      206 GGCCTTCACTAATTC 192

RESULT 13
LOCUS   BY030621/c
DEFINITION BY030621 RIKEN full-length enriched, pooled tissues, 1 cell embryo,
etc. Mus musculus cDNA clone I0C0013L23 5', mRNA sequence.
ACCESSION BY030621
VERSION   BY030621.1 GI:26136064
KEYWORDS EST.
SOURCE    Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS   Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
          Nikaudo, N., Osafo, R., Saico, R., Suzuki, H., Yamanaka, I.,
          Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
          Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
          Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
          Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
          Chothea, C., Corbani, L.E., Cousins, S., Dalia, E., Dragani, T.A.,
          Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
          Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
          Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
          Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
          Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
          Maltas, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
          Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, S.,
          Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
          Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
          Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
          Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
          Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
          Wells, C., Wilming, L.G., Wyszewski, B., Yang, Y., Yanagisawa, M., Yang, I.,
          Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
          Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
          Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
          Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
          Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
          Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
          Rogers, J., Birney, E. and Hayashizaki, Y.
          Analysis of the mouse transcriptome based on functional annotation
          of 60,770 full-length cDNAs
          Nature 420, 563-573 (2002)
          22354683
          PUBMED 12466851
          COMMENT Contact: Yoshihide Hayashizaki
          Laboratory for Genome Exploration Research Group, RIKEN Genomic
          Sciences Center (GSC), Yokohama Institute
          The Institute of Physical and Chemical Research (RIKEN)
          1-7-22 Suihito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          Tel: 81-45-503-9222
          Fax: 81-45-503-9216
          Email: genome-res@gsc.riken.go.jp,
          URL: http://genome.gsc.riken.go.jp/
          Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
          Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
          Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
          Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

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Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muranatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
Location/Qualifiers
source          1..449
                /organism="Mus musculus"
                /mol_type="mRNA"
                /db_xref="taxon:10090"
                /clone_lib="I0C0013L23"
                /clone_lib="RIKEN full-length enriched, pooled tissues, 1
                cell embryo, etc."
                /note="pooled tissues: (dev stage=1 cell
                embryo, sex=mix; cell_type=1 cell), (dev stage=3 cells
                embryo, sex=mix; cell_type=3 cells), (dev stage=4 cells
                embryo, sex=mix; cell_type=4
                cells), (dev stage=mouse, tissue type=whole
                body, sex=mix; cell_type=mouse), (dev stage=5 days
                embryo, tissue type=whole body, sex=mix), (dev stage=5 days
                embryo, tissue type=whole body, sex=mix)"

ORIGIN

Query Match      100.0%; Score 15; DB 13; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GGCCTTCACTAATTC 15
        |||
Db      387 GGCCTTCACTAATTC 373

RESULT 14
LOCUS   CG591152/c
DEFINITION CG591152 Mus musculus 129Sv/Ev Mus musculus genomic clone
OST245409, genomic survey sequence.
ACCESSION CG591152
VERSION   CG591152.1 GI:37398758
KEYWORDS GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS   Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          1 (bases 1 to 453)
          Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
          Pigott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
          Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
          Key, B.W. Jr., Kipp, P., Kohlhaufl, B., Ma, Z.-Q., Markesich, D.,
          Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
          Sparks, M.J., Van Sligtenhorst, I., Vogel, F., Waake, W., Xu, N.,
          Zhu, Q., Person, C. and Sands, A.T.
          Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
          screen to identify potential targets for therapeutic intervention
          Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
          JOURNAL
          COMMENT Contact: Zambrowicz BP
          OmniBank
          Lexicon Genetics Incorporated

```


4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES

source
1..453
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="129SV/EV"
/db_xref="taxon:10090"
/clone="OST245409"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129SV/Ev"

ORIGIN

Query Match 100.0%; Score 15; DB 29; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACCTAATTC 15
|||||

Db 222 GGCTTCACCTAATTC 208
|||||

RESULT 15

EX475529/c

LOCUS

DEFINITION BX475529 454 bp mRNA linear EST 04-SEP-2003
DKFZp686D04178 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

ACCESSION

VERSION BX475529

KEYWORDS

SOURCE EST.

ORGANISM

Homo sapiens (human)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2003)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by Olagen (Hilden/Germany) within the cDNA sequencing

consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp686D04178) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1..454

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686D04178"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: hlcc3)"

/note="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;

cDNA-collection"

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACCTAATTC 15
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Db 444 GGCTTCACCTAATTC 430

Search completed: March 21, 2004, 23:22:35
Job time : 2424 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 20:52:14 ; Search time 53.5 Seconds
(without alignments)
155.594 Million cell updates/sec

Title: US-09-260-624A-2

Perfect score: 15

Sequence: 1 cgtatgcacagatctg 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	4	US-09-454-495-3
2	15	100.0	2229	4	US-09-454-495-1
3	13.4	89.3	213	4	US-09-328-352-2112
4	13.4	89.3	1284	4	US-09-328-352-2004
5	13.4	89.3	1554	1	US-08-463-115-3
6	13.4	89.3	1554	1	US-08-465-388-3
7	13.4	89.3	41171	4	US-08-311-731A-122
8	13.4	89.3	116592	4	US-09-818-512-3
9	13	86.7	1170	4	US-09-491-577-49
10	13	86.7	2787	4	US-09-328-352-977
11	13	86.7	161652	4	US-09-497-855A-40
12	12.4	82.7	30	3	US-08-790-963-35
13	12.4	82.7	30	3	US-09-371-774-35
14	12.4	82.7	261	4	US-09-313-294A-2283
15	12.4	82.7	261	4	US-09-313-294A-2291
16	12.4	82.7	263	4	US-09-976-594-132
17	12.4	82.7	285	4	US-09-313-294A-3505
18	12.4	82.7	480	4	US-09-621-976-13863
19	12.4	82.7	493	4	US-09-621-976-2143
20	12.4	82.7	522	4	US-09-543-681A-1868
21	12.4	82.7	631	4	US-09-833-381-1443
22	12.4	82.7	819	4	US-09-543-681A-1839
23	12.4	82.7	1002	3	US-09-267-031-3
24	12.4	82.7	1167	4	US-09-134-001C-2365
25	12.4	82.7	1224	4	US-09-489-039A-6179
26	12.4	82.7	1276	4	US-09-023-655-705
27	12.4	82.7	2247	4	US-09-710-099-15

28	12.4	82.7	2436	4	US-08-983-275-1	Sequence 1, Appli
29	12.4	82.7	2760	2	US-08-788-674-6	Sequence 6, Appli
30	12.4	82.7	2830	4	US-09-221-017B-730	Sequence 730, App
31	12.4	82.7	3025	4	US-08-961-527-168	Sequence 168, App
32	12.4	82.7	3060	4	US-09-543-681A-275	Sequence 275, App
33	12.4	82.7	3486	4	US-09-543-681A-2314	Sequence 2314, Ap
34	12.4	82.7	4757	1	US-07-865-662F-12	Sequence 12, Appl
35	12.4	82.7	4757	3	US-08-374-219B-12	Sequence 12, Appl
36	12.4	82.7	8351	1	US-08-198-446B-14	Sequence 14, Appl
37	12.4	82.7	8351	2	US-08-870-693-14	Sequence 14, Appl
38	12.4	82.7	9511	1	US-07-925-695-6	Sequence 6, Appli
39	12.4	82.7	9511	1	US-07-925-695-7	Sequence 7, Appli
40	12.4	82.7	36470	4	US-08-311-731A-123	Sequence 123, App
41	12.4	82.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
42	12.4	82.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
43	12	80.0	161	4	US-09-621-976-19202	Sequence 19202, A
44	12	80.0	277	4	US-09-313-294A-842	Sequence 842, App
45	12	80.0	378	4	US-09-288-143-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-454-495-3
; Sequence 3, Application US/09454495
; Patent No. 6576759
; GENERAL INFORMATION:
; APPLICANT: Reddy, Gurucharan
; APPLICANT: Zeng, Hong
; APPLICANT: Vallerga, Anne
; TITLE OF INVENTION: NOVEL ANTISENSE INHIBITION OF RAD51
; FILE REFERENCE: A-67649-1/RMS/DAV/JJD
; CURRENT APPLICATION NUMBER: US/09/454,495
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/119,578
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic.
US-09-454-495-3

Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGCACAGATCTG 15
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Db 1 CGTATGCACAGATCTG 15

RESULT 2
US-09-454-495-1/c
; Sequence 1, Application US/09454495
; Patent No. 6576759
; GENERAL INFORMATION:
; APPLICANT: Reddy, Gurucharan
; APPLICANT: Zeng, Hong
; APPLICANT: Vallerga, Anne
; APPLICANT: Zarlino, David A.
; TITLE OF INVENTION: NOVEL ANTISENSE INHIBITION OF RAD51
; FILE REFERENCE: A-67649-1/RMS/DAV/JJD
; CURRENT APPLICATION NUMBER: US/09/454,495
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/119,578
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 10

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-454-495-1

Query Match      100.0%; Score 15; DB 4; Length 2229;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      1758 CGTATGACAGATCTG 1744

RESULT 3
US-09-328-352-2112
; Sequence 2112, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2112
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2112

Query Match      89.3%; Score 13.4; DB 4; Length 213;
Best Local Similarity 93.3%; Pred. No. 75;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      103 CGTATGAAGATCTG 117

RESULT 4
US-09-328-352-2004/c
; Sequence 2004, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2004
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2004

Query Match      89.3%; Score 13.4; DB 4; Length 1284;
Best Local Similarity 93.3%; Pred. No. 93;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      31 CGTATGAAGATCTG 17

RESULT 5
US-08-463-115-3/c
; Sequence 3, Application US/08463115
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; Patent No. 5703221
; GENERAL INFORMATION:
; APPLICANT: WILLIAM JOHN MARTIN
; TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
; TITLE OF INVENTION: AND RELATED VACCINES
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,115
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/157,811
; FILING DATE: No. 5703221, September 23, 1993
; APPLICATION NUMBER: 07/887,502
; FILING DATE: May 22, 1992
; APPLICATION NUMBER: 07/704,814
; FILING DATE: May 23, 1991
; APPLICATION NUMBER: 07/763,039
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburs, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 213/301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1554 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-463-115-3

Query Match      89.3%; Score 13.4; DB 1; Length 1554;
Best Local Similarity 93.3%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      987 CGTATGACCGATCTG 973

RESULT 6
US-08-465-368-3/c
; Sequence 3, Application US/08465388
; Patent No. 5753488
; GENERAL INFORMATION:
; APPLICANT: WILLIAM JOHN MARTIN
; TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
; TITLE OF INVENTION: AND RELATED VACCINES
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
```

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; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,388
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application Four
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/157,811
; FILING DATE: No. 575348ember 23, 1993
; APPLICATION NUMBER: 07/887,502
; FILING DATE: May 22, 1992
; APPLICATION NUMBER: 07/704,814
; FILING DATE: May 23, 1991
; APPLICATION NUMBER: 07/763,039
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 213/300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1554 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-465-388-3
;
Query Match      89.3%; Score 13.4; DB 1; Length 1554;
Best Local Similarity 93.3%; Pred.No. 95;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      .      1 CGTATGACAGATCTG 15
Db      .      987 CGTATGCCGATCTG 973

RESULT 7
US-08-311-731A-122
; Sequence 122, Application US/08311731A
; Patent No. 6583256
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0. Version #1.125

```

APPLICANT: Kim, Hunhyong
APPLICANT: Clyne, Peter J.
APPLICANT: Warr, Coral G.
TITLE OF INVENTION: No. 6610511el Family of Odorant Receptor Genes in Drosophila
FILE REFERENCE: 44574-5061-US
CURRENT APPLICATION NUMBER: US/09/491,577
CURRENT FILING DATE: 2000-01-25
EARLIER APPLICATION NUMBER: US 60/117,132
EARLIER FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
LENGTH: 1170
TYPE: DNA
ORGANISM: Drosophila melanogaster
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1170)
OTHER INFORMATION: DOR 85A.1
US-09-491-577-49

Query Match 86.7%; Score 13; DB 4; Length 1170;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TATGACGATCTG 15
|||||
DB 1107 TATGACGATCTG 1119

RESULT 10
US-09-328-352-977
Sequence 977, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 977
LENGTH: 2787
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-977

Query Match 86.7%; Score 13; DB 4; Length 2787;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACGATC 13
|||||
DB 2107 CGTATGACGATC 2119

RESULT 11
US-09-497-855A-40/c
Sequence 40, Application US/09497855A
Patent No. 6605432
GENERAL INFORMATION:
APPLICANT: Huang, Tim
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
FILE REFERENCE: UM01523
CURRENT APPLICATION NUMBER: US/09/497,855A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/120,592
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/118,760
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.0

SEQ ID NO 40
LENGTH: 161652
TYPE: DNA
ORGANISM: Homo sapiens;
US-09-497-855A-40

Query Match 86.7%; Score 13; DB 4; Length 161652;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TATGACGATCTG 15
|||||
DB 144144 TATGACGATCTG 144132

RESULT 12
US-08-790-963-35/c
Sequence 35, Application US/08790963
Patent No. 5837464
GENERAL INFORMATION:
APPLICANT: Daniel J. Capon
APPLICANT: Christos John Petropoulos
TITLE OF INVENTION: Compositions And Methods For
TITLE OF INVENTION: Determining Anti-viral Drug Susceptibility And
TITLE OF INVENTION: Resistance
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,963
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50130-B/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-790-963-35

Query Match 82.7%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTATGACGATCTG 15
|||||
DB 19 GTATGACGATCTG 6

RESULT 13
US-09-371-774-35/c
Sequence 35, Application US/09371774
Patent No. 6242187
GENERAL INFORMATION:
APPLICANT: Daniel J. Capon

Christos John Petropoulos
 TITLE OF INVENTION: Compositions And Methods For
 Determining Anti-viral Drug Susceptibility And
 Resistance And Anti-viral Drug Screening
 NUMBER OF SEQUENCES: 105
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version#1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/371,774
 FILING DATE: 10-Aug-1999
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 50130-F/JPW/CMR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0526
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 35:
 US-09-371-774-35

Query Match 82.7%; Score 12.4; DB 3; Length 30;
 Best Local Similarity 92.9%; Pred. No. 2.3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTATGACAGATCTG 15
 Db 19 GTATGACAGATCTG 6

RESULT 14
 US-09-313-294A-2283/C
 ; Sequence 2283, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalgudi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 2283
 ; LENGTH: 261
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6476212 700552426H1
 US-09-313-294A-2283

Query Match 82.7%; Score 12.4; DB 4; Length 261;
 Best Local Similarity 92.9%; Pred. No. 3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-09-313-294A-2291/C
 ; Sequence 2291, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalgudi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 2291
 ; LENGTH: 261
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6476212 700552437H1
 US-09-313-294A-2291

Query Match 82.7%; Score 12.4; DB 4; Length 261;
 Best Local Similarity 92.9%; Pred. No. 3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCT 14
 Db 71 CGTATGACAGATCT 58

RESULT 15
 US-09-313-294A-2291/C
 ; Sequence 2291, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalgudi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 2291
 ; LENGTH: 261
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6476212 700552437H1
 US-09-313-294A-2291

Query Match 82.7%; Score 12.4; DB 4; Length 261;
 Best Local Similarity 92.9%; Pred. No. 3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: March 21, 2004, 23:24:42
 Job time : 65.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 18:17:32 ; Search time 282 Seconds
(without alignments)
225.968 Million cell updates/sec

Title: US-09-260-624A-2

Perfect score: 15
Sequence: 1 cgtatgacagatctg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N Geneseq 29Jan04:*
- 1: Geneseqn1980as:*
 - 2: Geneseqn1990as:*
 - 3: Geneseqn2000as:*
 - 4: Geneseqn2001as:*
 - 5: Geneseqn2001bs:*
 - 6: Geneseqn2002as:*
 - 7: Geneseqn2003as:*
 - 8: Geneseqn2003bs:*
 - 9: Geneseqn2003cs:*
 - 10: Geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	3	AAA37713 Human Rad
2	15	100.0	15	4	AAS01195 Human RAD
3	15	100.0	15	4	AAS01204 Human RAD
4	15	100.0	15	6	AA43241 Antisense
5	15	100.0	1024	7	AB283420 Toxicolog
6	15	100.0	1408	2	AAG91761 Mouse Rad
7	15	100.0	1682	2	AAG91763 Mouse gen
8	15	100.0	1755	2	AAQ64088 Human Rad
9	15	100.0	2229	3	AAA37710 Human Rad
10	15	100.0	2228	4	AAS01209 Human RAD
11	14	93.3	470	7	AB223355 Nucleotid
12	14	93.3	510	4	AAB28846 Drosophil
13	14	93.3	513	4	AAB29139 Drosophil
14	14	93.3	649	3	AAFI4202 Aspergill
15	14	93.3	1017	6	ABK72962 Bacillus
16	14	93.3	2684	4	ABL25830 Drosophil
17	14	93.3	3630	4	ABL20510 Drosophil
18	14	93.3	3804	4	ABL20512 Drosophil
19	14	93.3	4053	4	ABL20514 Drosophil
20	14	93.3	5870	4	ABL12010 Drosophil
21	14	93.3	6128	4	ABL12010 Drosophil
22	13.4	89.3	45	6	ABA98655 T-vector-
23	13.4	89.3	183	6	ABA98646 Fragment

24	13.4	89.3	198	6	ABA98660 Fragment
25	13.4	89.3	213	8	ADA30825 DNA encod
26	13.4	89.3	251	3	AAC21220 Human sec
27	13.4	89.3	373	4	AAS5056 Human imm
28	13.4	89.3	398	3	AAB30637 Human col
29	13.4	89.3	410	7	ABX54935 Bovine ES
30	13.4	89.3	783	4	AAB30869 Human cDN
31	13.4	89.3	1284	8	ADA30717 DNA encod
32	13.4	89.3	1554	2	AAV11950 Cytonegal
33	13.4	89.3	1554	2	AAV10137 CMV nucle
34	13.4	89.3	2002	4	AAH45403 Human cDN
35	13.4	89.3	2003	6	ABK87929 Human cer
36	13.4	89.3	2118	4	AAF30809 Human cer
37	13.4	89.3	2118	6	ABK90633 DNA encod
38	13.4	89.3	4649	9	ADB69161 C. neofo
39	13.4	89.3	5236	6	ABK93703 Human sig
40	13.4	89.3	5920	9	ADA48199 Human gen
41	13.4	89.3	8173	4	AAK64969 Human imm
42	13.4	89.3	8173	4	AAS28231 Genomic s
43	13.4	89.3	8350	7	ADA05805 Human NOV
44	13.4	89.3	8350	7	ADA05799 Human NOV
45	13.4	89.3	8487	6	AB233756 Human TRI

ALIGNMENTS

RESULT 1
AAA37713

ID AAA37713 standard; DNA; 15 BP.

AC AAA37713;

DT 22-NOV-2000 (first entry)

XX Human Rad51 antisense inhibitor AS2.

XX Antisense inhibitor; human; Rad51; cell proliferation; cancer survival;
XX radiation sensitivity; therapy; AS2; ss.

OS Homo sapiens.

XX WO200047231-A2.

PD 17-AUG-2000.

XX 03-FEB-2000; 2000WO-US002881.

XX 10-FEB-1999; 99US-0119578P.

PR 06-DEC-1999; 99US-00454495.

XX (PANG-) PANGENE CORP.

XX Reddy G;

XX WPI; 2000-506091/45.

XX Inhibiting cell proliferation useful for cancer therapy, comprises
administering Rad51 inhibitor in vivo.

XX Example 1; Page 25; 42pp; English.

XX This sequence represents an antisense inhibitor of human Rad51,
designated AS2 (also referred to as RS1AS2). The antisense inhibitors can
be used in a method of the invention, for inhibiting cell proliferation.
They can also be used in methods for inducing sensitivity to radiation
and DNA damaging chemotherapeutics in an individual and in a method for
prolonging survival in an individual with cancer. The methods and
antisense molecules are useful for inhibiting cell proliferation,
especially cancerous cell proliferation, for inducing sensitivity to
radiation and DNA damaging chemotherapeutics in individuals and for
prolonging survival in an individual with cancer. Kits for carrying out
the methods may be used to diagnose and/or treat cancer and for


```

PN JP07143890-A.
XX
XX
PD 06-JUN-1995.
XX
XX 28-MAY-1993; 93JP-00127594.
XX
XX 28-MAY-1993; 93JP-00127594.
XX
XX (TOYM ) TOYOBO KK.
XX
XX WPI; 1995-236467/31.
XX P-PSDB; AAR78181.
XX
XX Structural gene encoding RAD51, used in production of RAD51 - used to
XX study drugs against diseases caused by DNA damage, e.g. by UV or X
XX radiation, and to improve efficiency if gene therapy targeting.
XX
XX Claim 1; Page 9-10; 19pp; Japanese.
XX
XX The present sequence, isolated from mouse cDNA and localised to the F1
XX region of chromosome 2, is a specific example of DNA coding for a RAD51
XX protein having the amino acid sequence in AAR78181. The RAD51 protein,
XX which contains an ATP-binding domain, is involved in DNA repair of
XX mismatched base pairs and site-specific recombination in antibody gene
XX rearrangements. The protein binds to double-stranded DNA to form a right-
XX handed helical nucleoprotein that extends (by 1.5 times) the pitch of B-
XX form DNA. As a result, the helix is unwound. The Rad51 gene and the
XX protein it encodes will be useful in designing drugs to treat diseases
XX associated with environmental DNA damage
XX
XX Sequence 1408 BP; 378 A; 318 C; 392 G; 320 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 15; DB 2; Length 1408;
XX Best Local Similarity 100.0%; Pred. No. 77;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CGTATGACAGATCTG 15
XX |||||
XX Db 605 CGTATGACAGATCTG 591
XX
XX RESULT 7
XX AAQ91763/c
XX ID AAQ91763 standard; cDNA to mRNA; 1682 BP.
XX
XX AC AAQ91763;
XX
XX 15-FEB-1996 (first entry)
XX
XX Human Rad51 gene, encodes protein involved in DNA repair.
XX
XX DNA mismatch repair; DNA recombination; site-specific; unwinding;
XX right-handed helical nucleoprotein; RAD51; human; recA; topoisomerase;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 215..1234
XX FT /*tag= a
XX FT /product= "RAD51"
XX
XX JP07143890-A.
XX
XX 06-JUN-1995.
XX
XX 28-MAY-1993; 93JP-00127594.
XX
XX 28-MAY-1993; 93JP-00127594.
XX
XX (TOYM ) TOYOBO KK.
XX
XX WPI; 1995-236467/31.
XX
XX Sequence 1755 BP; 485 A; 367 C; 467 G; 436 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 15; DB 2; Length 1682;
XX Best Local Similarity 100.0%; Pred. No. 78;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CGTATGACAGATCTG 15
XX |||||
XX Db 631 CGTATGACAGATCTG 617
XX
XX RESULT 8
XX AAQ64088/c
XX ID AAQ64088 standard; DNA; 1755 BP.
XX
XX AC AAQ64088;
XX
XX 13-FEB-1995 (first entry)
XX
XX Mouse gene participating in homologous recombination.
XX
XX Homologous recombination; Rad51; recA; gene therapy; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 176..1195
XX FT /*tag= a
XX
XX JP06141863-A.
XX
XX 24-MAY-1994.
XX
XX 10-NOV-1992; 92JP-00299714.
XX
XX 10-NOV-1992; 92JP-00299714.
XX
XX (MORI/) MORITA T.
XX (MATS/) MATSUSHIRO A.
XX
XX WPI; 1994-205025/25.
XX
XX P-PSDB; AAR54070.
XX
XX Mouse gene participating in homologous recombination reaction - useful
XX for improving the frequency of homologous recombination in gene therapy.
XX
XX Claim 4; Page 5-6; 8pp; Japanese.
XX
XX A mouse gene participating in homologous recombination, partic.
XX homologous to S. cerevisiae Rad51 and E. coli recA, is given in AAQ64088.
XX The gene improves the frequency of homologous recombination useful in
XX gene therapy and in the prepn. of disease model animals
XX
XX Sequence 1755 BP; 485 A; 367 C; 467 G; 436 T; 0 U; 0 Other;
XX

```

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Query Match      100.0%; Score 15; DB 2; Length 1755;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
DB 592 CGTATGACAGATCTG 578

RESULT 9
AAA37710/c
ID AAA37710 standard; mRNA; 2229 BP.
XX AAA37710;
AC
XX 22-NOV-2000 (first entry)
DT
XX Human Rad51 mRNA.
DE
XX Antisense inhibitor; human; Rad51; cell proliferation; cancer survival;
KW radiation sensitivity; therapy; AS9; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH misc_binding 1..15
FT /tag= a
FT /bound_moiety= "AS4"
FT misc_binding 158..177
FT /tag= b
FT /bound_moiety= "AS5"
FT CDS 233..1252
FT /tag= c
FT /product= "Rad51"
FT misc_binding 311..328
FT /tag= d
FT /bound_moiety= "AS3"
FT misc_binding 425..438
FT /tag= e
FT /bound_moiety= "AS1"
FT misc_binding 635..649
FT /tag= f
FT /bound_moiety= "AS2"
FT misc_binding 1524..1545
FT /tag= g
FT /bound_moiety= "AS6"
FT misc_binding 1881..1902
FT /tag= h
FT /bound_moiety= "AS7"
FT misc_binding 1911..1933
FT /tag= i
FT /bound_moiety= "AS8"
FT misc_binding 2038..2060
FT /tag= j
FT /bound_moiety= "AS9"
XX WO200047231-A2.
XX
XX 17-AUG-2000.
XX
XX 03-FEB-2000; 2000WO-US002881.
XX
XX 10-FEB-1999; 99US-0119578P.
XX 06-DEC-1999; 99US-00454495.
XX (PANG-) PANGENE CORP.
XX
XX Reddy G;
XX WPI; 2000-506091/45.
XX Inhibiting cell proliferation useful for cancer therapy, comprises
```

```
PT administering Rad51 inhibitor in vivo.
XX Disclosure; Fig 9b-9a; 42pp; English.
XX This sequence is the human Rad51 mRNA sequence. Antisense inhibitors of
CC this sequence can be used in a method for inhibiting cell proliferation.
CC They can also be used in methods for inducing sensitivity to radiation
CC and DNA damaging chemotherapeutics in an individual and in a method for
CC prolonging survival in an individual with cancer. The methods and
CC antisense molecules are useful for inhibiting cell proliferation,
CC especially cancerous cell proliferation, for inducing sensitivity to
CC radiation and DNA damaging chemotherapeutics in individuals and for
CC prolonging survival in an individual with cancer. Kits for carrying out
CC the methods may be used to diagnose and/or treat cancer and for
CC adjunctive therapy. Note: In the specification, the 3' end of this
CC sequence is shown in figure 9a, while the 5' end of this sequence is
CC given in figure 9b
XX
XX Sequence 2229 BP; 593 A; 472 C; 602 G; 562 T; 0 U; 0 Other;
SQ
Query Match      100.0%; Score 15; DB 3; Length 2229;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
DB 649 CGTATGACAGATCTG 635

RESULT 10
AAS01209/c
ID AAS01209 standard; cDNA; 2229 BP.
XX
XX AAS01209;
AC
XX 04-JUL-2001 (first entry)
DT
XX Human RAD51 cDNA sequence.
DE
XX Human; Rad51; antisense; drug screening; cancer; autoimmune disease;
KW arthritis; graft rejection; inflammatory bowel disease; surgery;
KW angioplasty; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH primer_bind complement(403..425)
FT /tag= a
FT /note= "Binds antisense oligonucleotide AS6"
FT primer_bind complement(761..782)
FT /tag= b
FT /note= "Binds antisense oligonucleotide AS7"
FT primer_bind complement(791..813)
FT /tag= c
FT /note= "Binds antisense oligonucleotide AS8"
FT primer_bind complement(918..940)
FT /tag= d
FT /note= "Binds antisense oligonucleotide AS9"
FT primer_bind complement(1110..1115)
FT /tag= e
FT /note= "Binds antisense oligonucleotide AS4"
FT primer_bind complement(1258..1267)
FT /tag= f
FT /note= "Binds antisense oligonucleotide AS5"
FT primer_bind complement(1413..1424)
FT /tag= g
FT /note= "Binds antisense oligonucleotide AS3"
FT primer_bind complement(1455..1468)
FT /tag= h
FT /note= "Binds antisense oligonucleotide AS1"
FT primer_bind complement(1745..1759)
FT /tag= i
FT /note= "Binds antisense oligonucleotide AS2"
FT
```

```

XX PN WC200119397-A1.
XX PD 22-MAR-2001.
XX PF 18-SEP-2000; 2000WO-US025838.
XX PR 17-SEP-1999; 99US-0154616P.
XX PR 06-DEC-1999; 99US-00455300.
XX PA (PANG-) PANGENE CORP.
XX PI Reddy G;
XX DR WPI; 2001-244704/25.
XX PT Inhibiting cell proliferation for treating arthritis, graft rejection,
XX PT inflammatory bowel disease, cancer, proliferation induced after medical
XX PT procedure, involves administering Rad51 antibody or its fragment to cell.
XX PS Disclosure; Fig 15; 102pp; English.
XX CC The sequence represents the coding sequence of human Rad51. Rad51 protein
XX CC is defective in repair of damaged DNA, genetic recombination and the
XX CC recombinational repair of DNA lesions, and plays a central role in
XX CC cancer. The sequence was used to design antisense oligonucleotides which
XX CC were used to study down-regulation of Rad51 protein in human brain,
XX CC breast and prostate cells. Inhibiting cell proliferation involves
XX CC administering to a cell a Rad51 antibody or its fragment. The Rad51
XX CC antibody or its fragment is useful for inhibiting cell proliferation, for
XX CC treating disease states such as cancer, autoimmune disease, arthritis,
XX CC graft rejection, inflammatory bowel disease, proliferation induced after
XX CC medical procedures such as surgery, angioplasty etc. in humans and
XX CC animals
XX SQ Sequence 2229 BP; 593 A; 472 C; 602 G; 562 T; 0 U; 0 Other;
Query Match 100.0%; Score 15; DB 4; Length 2229;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTATGACAGATCTG 15
DB 1758 CGTATGACAGATCTG 1744

RESULT 11
ABZ23355/c
ID ABZ23355 standard; cDNA; 470 BP.
AC ABZ23355;
AC ABZ23355;
DT 07-APR-2003 (first entry)
DE Nucleotide sequence of a fragment of porcine RAD51 cDNA.
XX Antigenic determinant; immunotolerance; cell therapy; liver condition;
XX xenotransplantation; heart condition; pancreatic condition;
XX kidney condition; lung condition; RAD51; ss.
XX Sus sp.
XX WC200292791-A1.
XX 21-NOV-2002.
XX 14-MAY-2002; 2002WO-US015307.
XX 14-MAY-2001; 2001US-0291394P.
XX 13-AUG-2001; 2001US-0312125P.
XX 21-MAR-2002; 2002US-0367090P.
XX (STEL-) STELL.
XX PA

XX PI Liljedahl M, Marcantonio D, Aspland SE;
XX DR WPI; 2003-120679/11.
XX PF Novel genetically engineered cell in which a gene comprising an antigenic
XX PT determinant recognized by a recipient organism has been disrupted, useful
XX PT in cell therapy or xenotransplantation.
XX PR Example 9; Page 44-45; 97pp; English.
XX CC The specification describes genetically engineered cell in which at least
XX CC one gene encoding a polypeptide comprising an antigenic determinant which
XX CC is recognized by a desired recipient organism or at least one gene which
XX CC encodes a protein associated with the synthesis of a molecule comprising
XX CC the antigenic determinant has been disrupted. The genetically engineered
XX CC cell has a reduced level of immunogenicity in the recipient and can be
XX CC safely transplanted across species. It reduces the amount of medication
XX CC required to induce a state of immunotolerance in the host. The genetically
XX CC engineered cells of the invention are useful in cell therapy, or to
XX CC produce tissues or organs for use in xenotransplantation. They are useful
XX CC for treating heart conditions (e.g., valvular heart disease), liver
XX CC conditions (e.g., liver cirrhosis), pancreatic conditions (e.g.,
XX CC diabetes), kidney conditions (e.g., primary glomerulonephritis), lung
XX CC conditions (e.g., cystic fibrosis), Alzheimer's disease, stroke,
XX CC Parkinson's disease, cataracts and Creutzfeldt-Jacob disease. The present
XX CC sequence represents a PCR-amplified fragment of porcine RAD51 cDNA. The
XX CC fragment is used as a probe to identify homologous sequence to enhance
XX CC homologous recombination in the course of the invention
XX SQ Sequence 470 BP; 135 A; 112 C; 117 G; 106 T; 0 U; 0 Other;
Query Match 93.3%; Score 14; DB 7; Length 470;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTATGACAGATCTG 15
DB 224 GTATGACAGATCTG 211

RESULT 12
AAH28846/c
ID AAH28846 standard; DNA; 510 BP.
AC AAH28846;
AC AAH28846;
DT 17-JUL-2001 (first entry)
DE Drosophila melanogaster essential gene fragment, SEQ ID NO: 35.
XX Drosophila melanogaster; fruit fly; essential gene; screening assay;
XX pesticide; crop protection; chromosome 3; ds.
XX Drosophila melanogaster.
XX WO200118547-A1.
XX 15-MAR-2001.
XX 06-SEP-2000; 2000WO-GB003444.
XX 07-SEP-1999; 99GB-00021009.
XX (UNITU) UNIV GLASGOW.
XX Davies RW, Kaiser K, Yang MY;
XX WPI; 2001-281436/29.
XX Screening assays for used for identifying compounds having a
XX physiological effect on proteins identified as being essential.
XX PT

```

PS Claim 1; Page 136; 695pp; English.
 XX
 CC The present sequence is part of an essential gene from *Drosophila*
 CC melanogaster. Lack of expression of the protein encoded by this gene
 CC leads to a lethal or semi-lethal phenotype. The invention relates to 902
 CC nucleic acid sequences from genes encoding proteins which are thought to
 CC be essential, and to a screening assay for identifying compounds which
 CC have a physiological effect on these proteins. Suitable compounds are
 CC useful as pesticides and may be used in conjunction with other pesticides
 CC and herbicides for crop protection. The gene corresponding to the present
 CC sequence is located on chromosome 3
 XX
 SQ Sequence 510 BP; 155 A; 111 C; 108 G; 136 T; 0 U; 0 Other;
 Query Match 93.3%; Score 14; DB 4; Length 510;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GTATGACAGATCTG 15
 DB 316 GTATGACAGATCTG 303
 RESULT 13
 AAH29139
 ID AAH29139 standard; DNA; 513 BP.
 XX
 AC AAH29139;
 XX
 DT 17-JUL-2001 (first entry)
 XX
 DE *Drosophila melanogaster* essential gene fragment, SEQ ID NO: 328.
 XX
 KW *Drosophila melanogaster*; fruit fly; essential gene; screening assay;
 KW pesticide; crop protection; chromosome 3; ds.
 XX
 OS *Drosophila melanogaster*.
 XX
 PN WO200118547-A1.
 XX
 PD 15-MAR-2001.
 XX
 PF 06-SEP-2000; 2000WO-GB003444.
 XX
 PR 07-SEP-1999; 99GB-00021009.
 XX
 PA (UNITU) UNIV GLASGOW.
 XX
 PI Davies RW, Kaiser K, Yang MY;
 XX
 DR WPI; 2001-281436/29.
 XX
 FT Screening assays for used for identifying compounds having a
 FT physiological effect on proteins identified as being essential.
 XX
 PS Claim 1; Page 346; 695pp; English.
 XX
 CC The present sequence is part of an essential gene from *Drosophila*
 CC melanogaster. Lack of expression of the protein encoded by this gene
 CC leads to a lethal or semi-lethal phenotype. The invention relates to 902
 CC nucleic acid sequences from genes encoding proteins which are thought to
 CC be essential, and to a screening assay for identifying compounds which
 CC have a physiological effect on these proteins. Suitable compounds are
 CC useful as pesticides and may be used in conjunction with other pesticides
 CC and herbicides for crop protection. The gene corresponding to the present
 CC sequence is located on chromosome 3
 XX
 SQ Sequence 513 BP; 150 A; 94 C; 100 G; 169 T; 0 U; 0 Other;
 Query Match 93.3%; Score 14; DB 4; Length 513;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GTATGACAGATCTG 15
 DB 42 GTATGACAGATCTG 55
 RESULT 14
 AAF14202
 ID AAF14202 standard; cDNA; 649 BP.
 XX
 AC AAF14202;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE *Aspergillus cryzae* EST SEQ ID NO: 6725.
 XX
 KW Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; *Fusarium venenatum*; *Aspergillus niger*;
 KW *Aspergillus cryzae*; *Trichoderma reesei*; identification; recombination;
 KW culture condition; environmental stress; spore morphogenesis; ss.
 XX
 OS metabolic pathway engineering; catabolic pathway engineering; ss.
 XX
 PN WO200056762-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US007781.
 XX
 PR 22-MAR-1999; 99US-00273623.
 XX
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 XX
 DR WPI; 2000-594572/56.
 XX
 FT Monitoring differential expression of genes in filamentous fungal cells
 FT uses fluorescence-labeled nucleic acids isolated from the cells and a
 FT substrate of expressed sequence tags.
 XX
 PS Claim 88; Page 2744; 3161pp; English.
 XX
 CC The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring the
 CC global expression of genes from FF cells allows the production potential
 CC of the microorganisms to be improved. New genes may be discovered.
 CC possible functions of unknown open reading frames can be identified and
 CC gene copy number variation and stability can be monitored. The expression
 CC of genes can be used to study how FF cells adapt to changes in culture
 CC conditions, environmental stress, spore morphogenesis, recombination,
 CC metabolic or catabolic pathway engineering. Using ESTs provides several
 CC advantages over genomic or random cDNA clones including elimination of
 CC redundancy as one spot on an array equals one gene or open reading frame,
 CC and organisation of the microarrays based on function of the genes.
 CC products to facilitate analysis of the results. AAF07478 to AAF11247
 CC represents ESTs from *Fusarium venenatum*; AAF11248 to AAF11853 represents
 CC ESTs from *Aspergillus niger*; AAF11854 to AAF14878 represents ESTs from
 CC *Aspergillus cryzae*; and AAF14879 to AAF15337 represents ESTs from
 CC *Trichoderma reesei*, which are all specifically claimed in the present
 CC invention
 XX
 SQ Sequence 649 BP; 151 A; 166 C; 168 G; 164 T; 0 U; 0 Other;
 Query Match 93.3%; Score 14; DB 3; Length 649;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCT 14
| | | | | | | | | | | | | | | |
Db 401 CGTATGACAGATCT 414

RESULT 15
ABK72962
ID ABK72962 standard; DNA; 1017 BP.
XX
XX AC ABK72962;
XX
XX DT 13-AUG-2002 (first entry)
XX
XX DE Bacillus licheniformis genomic sequence tag (GST) #253.
XX
XX KW Differential gene expression; genomic sequenced tag; GST;
KW altered culture condition; environmental stress;
KW physiological provocation; ds.
XX
XX OS Bacillus licheniformis.
XX
XX PN WO200229113-A2.
XX
XX PD 11-APR-2002.
XX
XX PF 05-OCT-2001; 2001WO-US031437.
XX
XX PR 06-OCT-2000; 2000US-00680598.
XX PR 27-MAR-2001; 2001US-0279526P.
XX
XX PA (NOVO) NOVOZYMES BIOTECH INC.
XX PA (NOVO) NOVOZYMES AS.
XX
XX PI Berka R, Clausen IG;
XX
XX DR WPI; 2002-416684/44.
XX
XX PT Monitoring differential expression of several genes in first Bacillus
PT cell relative to expression of same genes in one or more second Bacillus
PT cells, by using substrate containing Bacillus genomic sequenced tag
PT array.
XX
XX PS Claim 4; SEQ ID NO 253; 200pp; English.
XX
XX CC The invention describes a method of monitoring differential expression of
CC genes in a first Bacillus cell relative to expression of the genes in
CC other Bacillus cells, comprising hybridising labelled nucleic acid probes
CC isolated from Bacillus cells to a substrate containing array of Bacillus
CC genomic sequenced tags (GST), examining the array, and determining
CC relative gene expression by an observed hybridisation reporter signal of
CC a spot in the array. The method is useful for measuring the expression of
CC genes in a first Bacillus cell relative to expression of the same genes
CC in one or more second Bacillus cells. The method is useful for monitoring
CC global expression of several genes from a Bacillus cell, discovering new
CC genes, identifying possible functions of unknown open reading frames and
CC monitoring gene copy number variation and stability. Monitoring changes
CC in expression of genes may be used to provide a representation of the way
CC in which Bacillus cells adapt to changes in culture conditions,
CC environmental stress or other physiological provocation. Extensive follow
CC up characterisation is unnecessary, when one spot on an array equals one
CC gene or one open reading frame, since sequence information is available.
CC This sequence represents a genomic sequence tag (GST) used in the method
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1017 BP; 296 A; 221 C; 296 G; 204 T; 0 U; 0 Other;

Query Match 93.3%; Score 14; DB 6; Length 1017;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCT 14
| | | | | | | | | | | | | | | |
Db 651 CGTATGACAGATCT 664

Search completed: March 21, 2004, 21:10:40
Job time : 287 secs

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OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 19:46:36 ; Search time 1531.5 Seconds
(without alignments)
424.516 Million cell updates/sec

Title: US-09-260-624A-2

Perfect score: 15
Sequence: 1 cgtatcacagatctg 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.or.*
21: em.ov.*
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23: em.pat.*
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30: em.htg.hum.*
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39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	15	100.0	15	6	BD271100	BD271100 Novel ant
2	15	100.0	15	6	AR343099	AR343099 Sequence
3	15	100.0	15	6	AX099905	AX099905 Sequence
c 4	15	100.0	15	6	AX099908	AX099908 Sequence
5	15	100.0	15	6	AX492790	AX492790 Sequence
c 6	15	100.0	357	6	E07534	E07534 Oligonucleo
c 7	15	100.0	425	9	AY425955	AY425955 Homo sapi
c 8	15	100.0	798	9	AF233739S4	AF233742 Homo sapi
c 9	15	100.0	1160	9	HS51RAD3	AF165090 Homo sapi
c 10	15	100.0	1408	6	E09402	E09402 RAD51 struc
c 11	15	100.0	1408	10	MUSRAD51A	DI3803 Mouse mRNA
c 12	15	100.0	1645	6	AX771463	AX771463 Sequence
c 13	15	100.0	1645	9	HUMRAD51B	DI3804 Human mRNA
c 14	15	100.0	1682	6	E09404	E09404 RAD51 struc
c 15	15	100.0	1745	10	MUSRAD51	DI3473 Mus muscu
c 16	15	100.0	1755	6	E07535	E07535 Clone pMR51
c 17	15	100.0	2121	10	BC027384	BC027384 Mus muscu
c 18	15	100.0	2229	6	BD271098	BD271098 Novel ant
c 19	15	100.0	2229	6	AR343097	AR343097 Sequence
c 20	15	100.0	2229	6	AX099913	AX099913 Sequence
c 21	15	100.0	2229	9	HUMRAD51	DI4134 Human mRNA
c 22	15	100.0	39521	9	AY196785	AY196785 Homo sapi
c 23	15	100.0	58572	2	AC090935	AC090935 Homo sapi
c 24	15	100.0	96678	9	HS47710A	AL096755 Human DNA
c 25	15	100.0	156608	2	AF004445	AP002445 Homo sapi
c 26	15	100.0	178248	9	AC012476	AC012476 Homo sapi
c 27	15	100.0	182430	2	AC118799	AC118799 Rattus no
c 28	15	100.0	189540	10	AL772264	AL772264 Mouse DNA
c 29	15	100.0	190512	2	AC140278	AC140278 Mus muscu
c 30	15	100.0	218553	2	AC079940	AC079940 Mus muscu
c 31	15	100.0	221086	9	AC090359	AC090359 Homo sapi
c 32	15	100.0	223408	2	AF001566	AP001566 Homo sapi
c 33	15	100.0	262126	2	AC098502	AC098502 Rattus no
c 34	14	93.3	280	8	HVU234491	AJ234491 Hordeum v
c 35	14	93.3	510	6	AX093911	AX093911 Sequence
c 36	14	93.3	513	6	AX094204	AX094204 Sequence
c 37	14	93.3	576	8	CNS0198P	BT011037 Drosophil
c 38	14	93.3	745	3	BT011037	BT011037 Drosophil
c 39	14	93.3	920	14	BHV4GF80	Z84818 Bovine herp
c 40	14	93.3	1017	6	AX431838	AX431838 Sequence
c 41	14	93.3	1020	10	CORAD51	Y08202 C.griseus m
c 42	14	93.3	1154	1	MSGAG	D16546 Mycobacteri
c 43	14	93.3	1182	1	MSGAG	D26187 Mycobacteri
c 44	14	93.3	1236	1	MAALANT	X63437 M.avium gen
c 45	14	93.3	1460	14	BHV4GENO	Z46507 Bovine herp

ALIGNMENTS

RESULT 1	BD271100	15 bp	DNA	linear	PAT 07-AUG-2003
LOCUS	BD271100	Novel antisense inhibition of Rad51.			
DEFINITION	BD271100	Novel antisense inhibition of Rad51.			
ACCESSION	BD271100.1	GI:33080868			
VERSION	BD271100.1	GI:33080868			
KEYWORDS	JP 2002536420-A/3.				
SOURCE	JP 2002536420-A/3.				
ORGANISM	synthetic construct				
	artificial sequences.				
REFERENCE	1 (bases 1 to 15)				
AUTHORS	Zeng,H., Reddy,G., Vallerga,A. and Zarling,D.A.				
TITLE	Novel antisense inhibition of Rad51				
JOURNAL	Patent: JP 2002536420-A 3 29-OCT-2002;				
	PANGENE CORP				

Pred. No. is the number of results predicted by chance to have a

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COMMENT      OS      Artificial Sequence
PN          JP 2002536420-A/3
PD          29-OCT-2002
PF          03-FEB-2000 JP 2000598182
PI          10-FEB-1999 US 60/119578.06-DEC-1999 US 09/454495 PI
PR          HONG ZENG, GURUCHARAN REDDY, ANNE VALLERGA, DAVID A ZARLING PC
A61K45/00, A61K31/7088, A61K48/00, A61P1/00, A61P19/02, A61P29/00, PC
A61P35/00
PC          A61P37/06, G01N33/50
CC          Description of Artificial Sequence: synthetic FH      Key
FT          Location/Qualifiers
FT          source
FT          1. .15
FT          Location/Qualifiers
FT          1. .15
FT          /organism="synthetic construct"
FT          /mol_type="genomic DNA"
FT          /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      1 CGTATGACAGATCTG 15

RESULT 2
AR343099
LOCUS      AR343099      15 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION      Sequence 3 from patent US 6576759.
ACCESSION      AR343099
VERSION      AR343099.1 GI:33738510
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Zeng, H., Reddy, G., VallerGA, A. and Zarling, D.A.
TITLE      Antisense inhibition of RAD51
JOURNAL      Patent: US 6576759-A 3 10-JUN-2003;
FEATURES
source
1. .15
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      1 CGTATGACAGATCTG 15

RESULT 3
AX099905
LOCUS      AX099905      15 bp      DNA      linear      PAT 02-APR-2001
DEFINITION      Sequence 8 from Patent WO0119397.
ACCESSION      AX099905
VERSION      AX099905.1 GI:13538931
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
AUTHORS      Reddy, G.
TITLE      Methods and compositions utilizing rad51
JOURNAL      Patent: WO 0119397-A 8 22-MAR-2001;
Pangene Corporation (US)

FEATURES
source
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide"

ORIGIN
Query Match      100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      1 CGTATGACAGATCTG 15

RESULT 4
AX099908/c
LOCUS      AX099908      15 bp      DNA      linear      PAT 02-APR-2001
DEFINITION      Sequence 11 from Patent WO0119397.
ACCESSION      AX099908
VERSION      AX099908.1 GI:13538934
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
AUTHORS      Reddy, G.
TITLE      Methods and compositions utilizing rad51
JOURNAL      Patent: WO 0119397-A 11 22-MAR-2001;
Pangene Corporation (US)
FEATURES
source
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide"

ORIGIN
Query Match      100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      1 CGTATGACAGATCTG 15

RESULT 5
AX492790
LOCUS      AX492790      15 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION      Sequence 2 from Patent WO02058738.
ACCESSION      AX492790
VERSION      AX492790.1 GI:23338473
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
AUTHORS      Zarling, D.A. and Reddy, G.
TITLE      Use of rad51 inhibitors for p53 gene therapy
JOURNAL      Patent: WO 02058738-A 2 01-AUG-2002;
PANGENE CORP (US)
FEATURES
source
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide"

ORIGIN
Query Match      100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      15 CGTATGACAGATCTG 1

```



```

Best Local Similarity 100.0%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
    |||||
Db 1 CGTATGACAGATCTG 15

RESULT 6
E07534/c
LOCUS E07534 357 bp RNA linear PAT 29-SEP-1997
DEFINITION Oligonucleotide including all of the base sequences possible to
            coding the important amino acid sequences in Rad 51.
ACCESSION E07534
VERSION E07534.1 GI:2175669
KEYWORDS JP 1994141863-A/3.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 357)
AUTHORS Morita,T. and Matsushiro,A.
TITLE MURINE GENE PARTICIPATING IN HOMOLOGOUS RECOMBINING REACTION
JOURNAL Patent: JP 1994141863-A 3 24-MAY-1994;
COMMENT MORITA TAKASHI, MATSUSHIRO AIZO
OS None
OC Artificial sequences.
PN JP 1994141863-A/3
PD 24-MAY-1994
PF 10-NOV-1992 JP 1992299714
PI MORITA TAKASHI, MATSUSHIRO AIZO
PC C12N15/12,C12N1/19//C12Q1/68;
CC strandedness: Single;
CC topology: Linear;
FH Key
FT Location/Qualifiers
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Query Match 100.0%; Score 15; DB 6; Length 357;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
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Db 36 CGTATGACAGATCTG 22

RESULT 7
AY425955/c
LOCUS AY425955 425 bp mRNA linear PRI 03-NOV-2003
DEFINITION Homo sapiens Rad51 mRNA, partial cds, alternatively spliced.
ACCESSION AY425955
VERSION AY425955.1 GI:38017104
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 425)
            Venables,J.P.
REFERENCE Alternative splicing in the testes
AUTHORS Unpublished
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 425)
AUTHORS Venables,J.P.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2003) Institute of Human Genetics, Newcastle
            University, International Centre for Life, Central Parkway,

Newcastle upon Tyne, England NE1 3BZ, UK
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
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Db 384 CGTATGACAGATCTG 370

RESULT 8
AF233739S4/c
LOCUS AF233739S4 798 bp DNA linear PRI 21-SEP-2000
DEFINITION Homo sapiens RAD51 gene, exon 5.
ACCESSION AF233742
VERSION AF233742.1 GI:7767550
KEYWORDS
SEGMENT 4 of 7
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 798)
            Ebbers,S.M. and Struwing,J.P.
REFERENCE Direct Submission
AUTHORS Submitted (09-FEB-2000) Laboratory of Population Genetics, National
            Cancer Institute, 41 Library Dr., Room D702, Bethesda, MD
            20892-5060, USA
            Location/Qualifiers
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            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
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            /number=5

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ORIGIN
Query Match 100.0%; Score 15; DB 9; Length 798;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
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Db 497 CGTATGACAGATCTG 483

RESULT 9
HSS1RAD3/c
LOCUS HSS1RAD3 1160 bp DNA linear PRI 25-JAN-2002
DEFINITION Homo sapiens Rad51 gene, exon 5.
ACCESSION AFL65090
VERSION AFL65090.1 GI:5733652
KEYWORDS
SEGMENT 3 of 7

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SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1160)
 AUTHORS Schmutte, C., Tomblin, G., Rhien, K., Sadoff, M.M., Schmutzler, R., von
 Deimling, A., and Fishel, R.
 TITLE Characterization of the human Rad51 genomic locus and examination
 of tumors with 15q14-15 loss of heterozygosity (LOH)
 JOURNAL Cancer Res. 59 (18), 4564-4569 (1999)
 MEDLINE 99421251
 PUBMED 10493508
 REFERENCE 2 (bases 1 to 1160)
 AUTHORS Schmutte, C., Tomblin, G., and Fishel, R.
 TITLE Direct Submission
 JOURNAL Submitted (05-JUL-1999) Kimmel Cancer Center, Thomas Jefferson
 University, 233 S. 10th St., BLSB933, Philadelphia, PA 19107, USA
 FEATURES source
 1. .1160
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 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTATGACAGATCTG 15
 Db 868 CGTATGACAGATCTG 854
 RESULT 10
 E09402/C
 LOCUS RAD51 structural gene. 1408 bp RNA linear PAT 29-SEP-1997
 DEFINITION E09402
 ACCESSION E09402.1 GI:22026029
 VERSION JP 1995143890-A/1
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1408)
 AUTHORS Shinohara, A., Nanao, N., Ogawa, H., and Ogawa, T.
 TITLE RAD51 STRUCTURE GENE
 JOURNAL Patent: JP 1995143890-A 1 06-JUN-1995;
 TOYOBO CO LTD
 COMMENT OS Mus musculus (mouse)
 PN JP 1995143890-A/1
 PD 06-JUN-1995
 PF 28-MAY-1993 JP 1993127594
 PI SHINOHARA AKIRA, NANAJO NORIKO, OGAWA HIDEYUKI, OGAWA TOMOKO
 PC C12N15/12, C12N1/19, C12N5/10, C12P21/02, (C12N1/19, C12R1:865), PC
 (C12P21/02,
 PC C12R1:865), (C12P21/02, C12R1:19), (C12P21/02, C12R1:91); CC
 strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC feature is identified by experimental;
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 FT source 1. .1408
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 FT misc_feature 1. .1408
 /note="A structural gene recombining DNA and

FT repairing DNA
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 1. .1408
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 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTATGACAGATCTG 15
 Db 605 CGTATGACAGATCTG 591
 RESULT 11
 MUSRAD51A/C
 LOCUS Mouse mRNA for RecA-like protein MmRad51, complete cds. 1408 bp mRNA linear ROD 29-MAY-2002
 DEFINITION Mouse mRNA for RecA-like protein MmRad51, complete cds.
 ACCESSION D13803
 VERSION D13803.1 GI:303702
 KEYWORDS ATPase; DNA repair; MmRad51; RecA-like protein; meiosis;
 recombination.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1408)
 AUTHORS Shinohara, A., Ogawa, H., Matsuda, Y., Ushio, N., Ikeo, K., and Ogawa, T.
 TITLE Cloning of human, mouse and fission yeast recombination genes
 homologous to RAD51 and recA
 JOURNAL Nat. Genet. 4 (3), 239-243 (1993)
 MEDLINE 93364417
 PUBMED 8358431
 REFERENCE 2 (bases 1 to 1408)
 AUTHORS Shinohara, A.
 TITLE Direct Submission
 JOURNAL Submitted (02-DEC-1992) Akira Shinohara, Faculty of Science, Osaka
 University, Department of Biology, Toyonaka, Osaka 560, Japan
 (E-mail: c62528@center.osaka-u.ac.jp, Tel:06-844-1151(ex.4305),
 Fax:06-841-2449)
 COMMENT Submitted (02-DEC-1992) to DDBJ by:
 Akira Shinohara
 Department of Biology
 Faculty of Science
 Osaka University
 1-1 Machikaneyama
 Toyonaka, Osaka 560
 Japan
 Phone: 06-844-1151 x4305
 Email: c62528@center.osaka-u.ac.jp
 Fax: 06-841-2449.
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ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 1408;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCTG 15
Db 605 CGTATGACAGATCTG 591

RESULT 12

AX771463/c AX771463 1645 bp DNA linear PAT 02-JUL-2003
LOCUS
DEFINITION Sequence 176 from Patent WO03004646.
ACCESSION AX771463
VERSION AX771463.1 GI:32438339

KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 O'Mahony, D.J., Byrne, D., Brayden, D., Lambkin, I. and Higgins, L.
Genetic analysis of Peyer's patches and M cells and methods and
compositions targeting Peyer's patches and M cell receptors
Patent: WO 03004646-A 176 16-JAN-2003;
ELAN CORPORATION, PIC (IE)

FEATURES

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Query Match 100.0%; Score 15; DB 6; Length 1645;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCTG 15
Db 628 CGTATGACAGATCTG 614

RESULT 13

HUMRAD51B/c HUMRAD51B 1645 bp mRNA linear PRI 29-MAY-2002
LOCUS
DEFINITION Human mRNA for RecA-like protein HsRad51, complete cds.

ACCESSION

DI3804
DI3804.1 GI:397826
VERSION
ATPase; DNA repair; HsRad51; RecA-like protein; meiosis;
recombination.

KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1645)
Shinohara, A., Ogawa, H., Matsuda, Y., Ushio, N., Ikeo, K. and Ogawa, T.
Cloning of human, mouse and fission yeast recombination genes
homologous to RAD51 and recA
Nat. Genet. 4 (3), 239-243 (1993)

JOURNAL

MEDLINE
PUBMED
8358431

REFERENCE

2 (bases 1 to 1645)
Shinohara, A.
AUTHORS
TITLE Direct Submission
JOURNAL
Submitted (02-DEC-1992) Akira Shinohara, Faculty of Science, Osaka

University, Department of Biology; Toyonaka, Osaka 560, Japan
(E-mail: c62528@center.osaka-u.ac.jp, Tel: 06-844-1151 (ex. 4305),
Fax: 06-841-2449)

On Sep 8, 1993 this sequence version replaced gi:303619.
Submitted (02-DEC-1992) to DDBJ by:

Akira Shinohara

Department of Biology

Faculty of Science

Osaka University

1-1 Machikaneyama

Toyonaka, Osaka 560

Japan

Phone: 06-844-1151 x4305

Email: c62528@center.osaka-u.ac.jp

Fax: 06-841-2449.

FEATURES

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Query Match 100.0%; Score 15; DB 9; Length 1645;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCTG 15

Db 628 CGTATGACAGATCTG 614

RESULT 14

E09404/c E09404 1682 bp RNA linear PAT 29-SEP-1997
LOCUS
DEFINITION RAD51 structural gene.

ACCESSION

E09404
E09404.1 GI:22026031
VERSION
JP 1995143890-A/3.
KEYWORDS
Homo sapiens (human)

SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1682)
Shinohara, A., Namajio, N., Ogawa, H. and Ogawa, T.

AUTHORS

RAD51 STRUCTURE GENE

TITLE

Patent: JP 1995143890-A 3 06-JUN-1995;

JOURNAL

TOYOBO CO LTD

COMMENT

OS Homo sapiens (human)

PN JP 1995143890-A/3

PD 06-JUN-1995

PI 28-MAY-1993 JP 1993127594

Submitted (02-DEC-1992) Akira Shinohara, Faculty of Science, Osaka

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PC      C12N15/12,C12N1/19,C12N5/10,C12P21/02,(C12N1/19,C12R1:865),PC
PC      (C12P21/02,(C12P21/02,C12R1:865),(C12P21/02,C12R1:91);CC
strandedness: Single;
CC      topology: Linear;
CC      hypothetical: No;
CC      anti-sense: No;
CC      Feature is identified by experimental;
FH      Key      Location/Qualifiers
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FT      DNA and repairs DNA damage".
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      631 CGTATGACAGATCTG 617
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RESULT 15
MUSRAD51/c
LOCUS      MUSRAD51      1745 bp      mRNA      linear      ROD 05-FEB-2003
DEFINITION      Mus musculus mRNA for Rad51 protein, complete cds.
ACCESSION      D13473
VERSION      D13473.1 GI:407348
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Morita,T., Yoshimura,Y., Yamamoto,A., Murata,K., Mori,M.,
Yamamoto,H. and Matsushiro,A.
A mouse homolog of the Escherichia coli recA and Saccharomyces
cerevisiae RAD51 genes
Proc. Natl. Acad. Sci. U.S.A. 90 (14), 6577-6580 (1993)
93342035
MEDLINE      8341671
PUBMED
REFERENCE      2 (bases 1 to 1745)
AUTHORS      Morita,T.
TITLE      Direct Submission
JOURNAL      Submitted (26-OCT-1992) Takashi Morita, Research Institute for
Microbial Diseases, Dept. of Microbial Genetics, Osaka Univ.; 3-1
Yamadaoka, Suita, Osaka 565, Japan (Tel.81-6-6877-5121(ex.3172),
Fax:81-6-6876-2678)
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LIVDSATALYRTDYSGRGELSAQMHLARFLMLRLADEFGVAVVITNQVVAQVDGA
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/gene="Rad51"
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      592 CGTATGACAGATCTG 578
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Search completed: March 21, 2004, 22:01:56
Job time : 1534.5 secs


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; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-454-495-1
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Best Local Similarity 100.0%; Pred. No. 21;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACATAATTC 15
Db 1548 GGCTTCACATAATTC 1534

RESULT 3
US-08-968-685A-9/c
; Sequence 9, Application US/08968685A
; Patent No. 6214981
; GENERAL INFORMATION:
; APPLICANT: TUCKER, KENNETH
; APPLICANT: PLOSILA, LAURA
; TITLE OF INVENTION: MORAXELLA CATARRHALIS OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN-106 POLYPEPTIDE, GENE SEQUENCE AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,685A
; FILING DATE: No. 6214981ember 12, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Baldwin, Geraldine P.
; REGISTRATION NUMBER: 31,232
; REFERENCE/DOCKET NUMBER: 7969-060
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-968-685A-9
Query Match 93.3%; Score 14; DB 3; Length 9542;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCTTCACATAATTC 15
Db 438 GGCTTCACATAATTC 425

RESULT 4
US-09-246-963A-6/c
; Sequence 6, Application US/09246963A
; Patent No. 6541684
; GENERAL INFORMATION:

```

```

; APPLICANT: Bowen, Benjamin A.
; APPLICANT: Chamberlin, Mark A.
; APPLICANT: Drummond, Bruce J.
; APPLICANT: McElver, John A.
; APPLICANT: Rothstein, Rodney J.
; TITLE OF INVENTION: Nucleotide Sequences Encoding Maize
; TITLE OF INVENTION: RAD51
; FILE REFERENCE: 033229/0750
; CURRENT APPLICATION NUMBER: US/09/246,963A
; CURRENT FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 60/074,745
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Zea mays
US-09-246-963A-6
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Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTTCACATAATTC 15
Db 210 GGCTTCACATAATTC 196

RESULT 5
US-09-328-352-1457/c
; Sequence 1457, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1457
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1457
Query Match 89.3%; Score 13.4; DB 4; Length 1029;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTTCACATAATTC 15
Db 96 GGCTTCACATAATTC 82

RESULT 6
US-09-329-796-2
; Sequence 2, Application US/09329796
; Patent No. 6231174
; GENERAL INFORMATION:
; APPLICANT: Ning Li
; APPLICANT: Changxin WU
; APPLICANT: Yaofeng ZHAO
; TITLE OF INVENTION: DNA MARKERS FOR PIG LITTER SIZE
; FILE REFERENCE: 064727.0104
; CURRENT APPLICATION NUMBER: US/09/329,796
; CURRENT FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: 60/088,963
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

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; LENGTH: 1181
; TYPE: DNA
; ORGANISM: Sus scrofa
US-09-329-796-2

Query Match 89.3%; Score 13.4; DB 3; Length 1181;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
|||||
DB 1165 GGCTTCACTAATTC 1179

RESULT 7

US-09-328-352-2749
; Sequence 2749, Application US/09328352
; Patent No. 6562958

; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2749

; LENGTH: 1479
; TYPE: DNA

; ORGANISM: Acinetobacter baumannii
US-09-328-352-2749

Query Match 89.3%; Score 13.4; DB 4; Length 1479;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
|||||
DB 1317 GGCTTCACTAATTC 1331

RESULT 8

US-09-246-963A-5/c

; Sequence 5, Application US/09246963A
; Patent No. 6541684

; GENERAL INFORMATION:
; APPLICANT: Bowen, Benjamin A.

; APPLICANT: Chamberlin, Mark A.
; APPLICANT: Drummond, Bruce J.

; APPLICANT: McElver, John A.
; APPLICANT: Rothstein, Rodney J.

; TITLE OF INVENTION: Nucleotide Sequences Encoding Maize
; FILE REFERENCE: PADI51

; CURRENT APPLICATION NUMBER: US/09/246,963A
; CURRENT FILING DATE: 1999-02-09

; PRIOR APPLICATION NUMBER: US 60/074,745
; PRIOR FILING DATE: 1998-02-13

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5
; LENGTH: 1574

; TYPE: DNA
; ORGANISM: Zea mays

; FEATURE:
; NAME/KEY: CDS

; LOCATION: (73)...(1092)
US-09-246-963A-5

Query Match 89.3%; Score 13.4; DB 4; Length 1574;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
|||||
DB 282 GGCTTCACTAATTC 268

RESULT 9

US-09-833-381-1020/c

; Sequence 1020, Application US/09833381
; Patent No. 6672186

; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1020
; LENGTH: 2139

; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: misc feature

; LOCATION: (1)...(2139)
; OTHER INFORMATION: n = A,T,C or G

US-09-833-381-1020

Query Match 89.3%; Score 13.4; DB 4; Length 2139;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
|||||
DB 1608 GGCTTCACTAATTC 1594

RESULT 10

US-09-374-135-1/c

; Sequence 1, Application US/09374135
; Patent No. 6277972

; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel E.

; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan

; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.

; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND

; SECRETED BY PROSTATE AND BLADDER CANCER CELLS
; FILE REFERENCE: 1703-017.US1

; CURRENT APPLICATION NUMBER: US/09/374,135
; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: 60/095,982
; PRIOR FILING DATE: 1998-08-10

; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 1
; LENGTH: 2639

; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-374-135-1

Query Match 89.3%; Score 13.4; DB 3; Length 2639;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
|||||
DB 766 GGCTTCACTAATTC 752

RESULT 11
US-09-976-594-679
; Sequence 679, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 679
; LENGTH: 2669
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1325741.20
; LOCATION: 196, 205-224
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-679
Query Match 89.3%; Score 13.4; DB 4; Length 2669;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
Db 71 GGCTTCTCAATTC 85
RESULT 12
US-09-620-312D-531/c
; Sequence 531, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yongsheng
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP22
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: PL_FL_Genes Version 1.0
; SEQ ID NO 531
; LENGTH: 2682
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)...(2286)
US-09-620-312D-531
Query Match 89.3%; Score 13.4; DB 4; Length 2682;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
Db 522 GGCTTCACTAATTC 508
RESULT 13
US-08-956-171E-358
; Sequence 358, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; FILING DATE: 20-Oct-1997
; APPLICATION NUMBER: US/08/956,171E
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 358:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 358:
US-08-956-171E-358
Query Match 89.3%; Score 13.4; DB 4; Length 3621;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
Db 1133 GGCTTCACTAATTC 1147

RESULT 14
US-08-516-859A-3/c
Sequence 3, Application US/08516859A
Patent No. 6069231
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5868 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 121..5278
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-586-472-3
Query Match 89.3%; Score 13.4; DB 3; Length 5868;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGCTTCACCTAATCC 15
Db 5333 GGCTTCACCTGATCC 5319
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Job time : 61.5 secs

US-08-516-859A-3
Query Match 89.3%; Score 13.4; DB 3; Length 5868;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGCTTCACCTAATCC 15
Db 5333 GGCTTCACCTGATCC 5319
RESULT 15
US-09-586-472-3/c
Sequence 3, Application US/09586472
Patent No. 6323335
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA

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OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 18:17:32 ; Search time 282 Seconds
(without alignments)
225.968 Million cell updates/sec

Title: US-09-260-624A-1
Perfect score: 15
Sequence: 1 gggttcactaatcc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373663 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N Geneseq_29Jan04:*
- 1: Geneseqn1980s:*
 - 2: Geneseqn1990s:*
 - 3: Geneseqn2000s:*
 - 4: Geneseqn2001as:*
 - 5: Geneseqn2001bs:*
 - 6: Geneseqn2002s:*
 - 7: Geneseqn2003as:*
 - 8: Geneseqn2003bs:*
 - 9: Geneseqn2003cs:*
 - 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Match	Length	DB ID	Description
		Score	Match				
1	15	100.0	15	3	AAA37712	Aaa37712 Human Rad	
2	15	100.0	15	4	AA501203	Aa501203 Human RAD	
3	15	100.0	15	4	AA501194	Aa501194 Human RAD	
4	15	100.0	15	6	AA433240	Aa433240 Antisense	
5	15	100.0	20	4	AA559439	Aaf59439 Human Rad	
6	15	100.0	1024	7	AB283420	Ab283420 Toxicolog	
7	15	100.0	1408	2	Aa911761	Aa911761 Mouse Rad	
8	15	100.0	1682	2	Aa911763	Aa911763 Human Rad	
9	15	100.0	1755	2	AaQ64088	AaQ64088 Mouse Gen	
10	15	100.0	2229	3	AA337710	Aa337710 Human RAD	
11	15	100.0	2229	3	AA501209	Aa501209 Human RAD	
12	15	100.0	21565	8	ADA02555	Ada02555 Mouse Ly6	
13	15	100.0	21565	9	AD722933	Ad722933 Mouse Ly6	
14	15	100.0	349980	5	AAH41223	Aah41223 Pyrococcus	
15	14	93.3	18	7	AB223353	Ab223353 Forward P	
16	14	93.3	379	4	AA189144	Aa189144 Human pol	
17	14	93.3	392	7	ABX62850	Abx62850 Arabidops	
18	14	93.3	470	7	AB223355	Ab223355 Nucleotid	
19	14	93.3	498	3	AA569207	Aa569207 Bacteriop	
20	14	93.3	582	5	ABV53858	Abv53858 Human pro	
21	14	93.3	1641	3	AA338441	Aa338441 Arabidops	
22	14	93.3	2000	6	AB215287	Ab215287 Arabidops	
23	14	93.3	2086	7	ADA53015	Ada53015 Human cod	

C	24	14	93.3	9542	5	RA004029	Aa04029 Moraxella
C	25	14	93.3	9542	7	ABX93525	Abx93525 DNA encod
C	26	14	93.3	56506	3	AA69168	Aa69168 Bacteriop
C	27	13.4	89.3	60	6	ABN40306	Abn40306 Human spl
C	28	13.4	89.3	101	6	ABK76843	Abk76843 Bacillus
C	29	13.4	89.3	132	2	AAQ76733	AaQ76733 Human gen
C	30	13.4	89.3	157	3	AAQ76733	AaQ76733 Human sec
C	31	13.4	89.3	300	7	ABZ40806	Abz40806 N. gonorr
C	32	13.4	89.3	305	2	AAV88366	Aav88366 EST clone
C	33	13.4	89.3	351	5	ABV51730	Abv51730 Human pro
C	34	13.4	89.3	367	4	ABA46368	Ab46368 Human bre
C	35	13.4	89.3	367	4	ABA26546	Ab26546 Probe H50
C	36	13.4	89.3	367	4	AAK30559	Aak30559 Human bon
C	37	13.4	89.3	367	4	ABS30224	Ab30224 Human liv
C	38	13.4	89.3	367	6	ABS05218	Ab505218 Human ORF
C	39	13.4	89.3	387	6	ABN78458	Abn78458 Human ORF
C	40	13.4	89.3	411	2	AAV88121	Aav88121 EST clone
C	41	13.4	89.3	416	3	AAQ09763	AaQ09763 Human sac
C	42	13.4	89.3	435	7	ACF03925	Acf03925 Rice endo
C	43	13.4	89.3	437	1	AAH81642	Aah81642 Human dif
C	44	13.4	89.3	465	5	AAH81642	Aah81642 Human dif
C	45	13.4	89.3	470	3	AAQ76558	AaQ76558 Human ORF

ALIGNMENTS

RESULT 1
AAA37712
ID AAA37712 standard; DNA; 15 BP.
XX
AC AAA37712;
XX
DT 22-NOV-2000 (first entry)
XX
DE Human Rad51 antisense inhibitor AS1.
XX
KW Antisense inhibitor; human; Rad51; cell proliferation; cancer survival;
KW radiation sensitivity; therapy; AS1; ss.
XX
OS Homo sapiens.
XX
PN WO200047231-A2.
XX
PD 17-AUG-2000.
XX
PF 03-FEB-2000; 2000WO-US002881.
XX
PR 10-FEB-1999; 99US-0119578P.
PR 06-DEC-1999; 99US-00454495.
XX
XX (PANG-) PANGENE CORP.
Reddy G;
WPI; 2000-506091/45.
PT Inhibiting cell proliferation useful for cancer therapy, comprises
administering Rad51 inhibitor in vivo.
Example 1; Page 25; 42pp; English.
This sequence represents an antisense inhibitor of human Rad51,
designated AS1 (also referred to as R51AS1). The antisense inhibitors can
be used in a method of the invention, for inhibiting cell proliferation.
They can also be used in methods for inducing sensitivity to radiation
and DNA damaging chemotherapeutics in an individual and in a method for
prolonging survival in an individual with cancer. The methods and
antisense molecules are useful for inhibiting cell proliferation,
especially cancerous cell proliferation, for inducing sensitivity to
radiation and DNA damaging chemotherapeutics in individuals and for
prolonging survival in an individual with cancer. Kits for carrying out
the methods may be used to diagnose and/or treat cancer and for

```

CC adjunctive therapy
XX Sequence 15 BP; 3 A; 5 C; 2 G; 5 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
DB 1 GGCTTCACTAATTC 15

RESULT 2
AAS01203/c
ID AAS01203 standard; cDNA; 15 BP.
XX AC AAS01203;
XX DT 04-JUL-2001 (first entry)
XX DE Human RAD51 sense oligonucleotide, S1.
XX Human; Rad51; drug screening; cancer; autoimmune disease; arthritis;
XX graft rejection; inflammatory bowel disease; surgery; angioplasty; ss.
XX Homo sapiens.
XX WO200119397-A1.
XX 22-MAR-2001.
XX PF 18-SEP-2000; 2000WO-US025838.
XX PR 17-SEP-1999; 99US-0154616P.
XX PR 06-DEC-1999; 99US-00455300.
XX PA (PANG-) PANGENE CORP.
XX PI Reddy G;
XX WPI; 2001-244704/25.
XX Inhibiting cell proliferation for treating arthritis, graft rejection,
XX inflammatory bowel disease, cancer, proliferation induced after medical
XX procedure, involves administering Rad51 antibody or its fragment to cell.
XX Example 6; Fig 16D; 102pp; English.
XX The sequence represents the human Rad51 sense oligonucleotide, S1. The
XX sense oligonucleotide is used to study down-regulation of Rad51 protein
XX in human brain, breast and prostate cells. Rad51 protein is defective in
XX repair of damaged DNA, genetic recombination and the recombinational
XX repair of DNA lesions, and plays a central role in cancer. Inhibiting
XX cell proliferation involves administering to a cell a Rad51 antibody or
XX its fragment. The Rad51 antibody or its fragment is useful for inhibiting
XX cell proliferation, for treating disease states such as cancer,
XX autoimmune disease, arthritis, graft rejection, inflammatory bowel
XX disease, proliferation induced after medical procedures such as surgery,
XX angioplasty etc. in humans and animals
XX Sequence 15 BP; 5 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
DB 15 GGCTTCACTAATTC 15

RESULT 3
AAS01194
ID AAS01194 standard; cDNA; 15 BP.
XX AC AAS01194;
XX DT 04-JUL-2001 (first entry)
XX DE Human RAD51 antisense oligonucleotide, AS1.
XX Human; Rad51; antisense; drug screening; cancer; autoimmune disease;
XX arthritis; graft rejection; inflammatory bowel disease; surgery;
XX angioplasty; ss.
XX Homo sapiens.
XX WO200119397-A1.
XX 22-MAR-2001.
XX PF 18-SEP-2000; 2000WO-US025838.
XX PR 17-SEP-1999; 99US-0154616P.
XX PR 06-DEC-1999; 99US-00455300.
XX PA (PANG-) PANGENE CORP.
XX PI Reddy G;
XX WPI; 2001-244704/25.
XX Inhibiting cell proliferation for treating arthritis, graft rejection,
XX inflammatory bowel disease, cancer, proliferation induced after medical
XX procedure, involves administering Rad51 antibody or its fragment to cell.
XX Example 6; Fig 16A; 102pp; English.
XX The sequence represents the human Rad51 antisense oligonucleotide, AS1.
XX The antisense oligonucleotide is used to study down-regulation of Rad51
XX protein in human brain, breast and prostate cells. Rad51 protein is
XX defective in repair of damaged DNA, genetic recombination and the
XX recombinational repair of DNA lesions, and plays a central role in
XX cancer. Inhibiting cell proliferation involves administering to a cell a
XX Rad51 antibody or its fragment. The Rad51 antibody or its fragment is
XX useful for inhibiting cell proliferation, for treating disease states
XX such as cancer, autoimmune disease, arthritis, graft rejection,
XX inflammatory bowel disease, proliferation induced after medical
XX procedures such as surgery, angioplasty etc. in humans and animals
XX Sequence 15 BP; 3 A; 5 C; 2 G; 5 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
DB 1 GGCTTCACTAATTC 15

RESULT 4
AAS01203/c
ID AAS01203 standard; cDNA; 15 BP.
XX AC AAS01203;
XX DT 14-NOV-2002 (first entry)
XX DE Antisense oligonucleotide R51AS1.
XX Tumour cell proliferation; Rad51 inhibitor; p53 protein; premature aging;
XX hyperproliferative disorder; Hodgkin's disease; squamous cell carcinoma;
XX leukaemia; autoimmune disease; cancer; graft rejection; angioplasty;
XX inflammatory bowel disease; immunosuppressive; gene therapy; arthritis;

```


PT radiation, and to improve efficiency if gene therapy targetting.

XX Claim 1; Page 15-16; 19pp; Japanese.

XX The present sequence, isolated from human cDNA and localised to the q
CC region of chromosome 15, is a specific example of DNA coding for a RAD51
CC protein having the amino acid sequence in AAR70183. The RAD51 protein,
CC which contains an ATP-binding domain, is involved in DNA repair of
CC mismatched base pairs and site-specific recombination in antibody gene
CC rearrangements. The protein binds to double-stranded DNA to form a right-
CC handed helical nucleoprotein that extends (by 1.5 times) the pitch of B-
CC form DNA. As a result, the helix is unwound. The Rad51 gene and the
CC protein it encodes will be useful in designing drugs to treat diseases
CC associated with environmental DNA damage

XX SQ Sequence 1682 BP; 477 A; 347 C; 456 G; 402 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 2; Length 1682;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

DB 421 GGCTTCACTAATTC 407

RESULT 9

AAQ64088/c

ID AAQ64088 standard; DNA; 1755 BP.

XX AAQ64088;

DT 13-FEB-1995 (first entry)

XX Mouse gene participating in homologous recombination.

DE Homologous recombination; Rad51; recA; gene therapy; ss.

XX Mus musculus.

XX Key Location/Qualifiers

FT CDS 176..1195

FT /*tag= a

XX JP06141863-A..

XX 24-MAY-1994.

PP 10-NOV-1992; 92JP-00299714.

PR 10-NOV-1992; 92JP-00299714.

XX (MORI/) MORITA T.

PA (MATS/) MATSUSHIRO A.

XX WPI; 1994-205025/25.

DR P-PSDB; AAR54070.

XX Mouse gene participating in homologous recombination reaction - useful
PT for improving the frequency of homologous recombination in gene therapy.

XX Claim 4; Page 5-6; 8pp; Japanese.

XX A mouse gene participating in homologous recombination, partic.
CC homologous to S. cerevisiae Rad51 and E. coli recA, is given in AAQ64088.
CC The gene improves the frequency of homologous recombination useful in
CC gene therapy and in the prepn. of disease model animals

XX SQ Sequence 1755 BP; 485 A; 367 C; 467 G; 436 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 2; Length 1755;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

DB 382 GGCTTCACTAATTC 368

RESULT 10

AAA37710/c

ID AAA37710 standard; mRNA; 2229 BP.

XX AAA37710;

XX 22-NOV-2000 (first entry)

XX Human Rad51 mRNA.

XX Antisense inhibitor; human; Rad51; cell proliferation; cancer survival;
KW radiation sensitivity; therapy; AS9; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT misc_binding 1..15

FT /*tag= a

FT /bound_moiety= "AS4"

FT misc_binding 158..177

FT /*tag= b

FT /bound_moiety= "AS5"

FT CDS 233..1252

FT /*tag= c

FT /product= "Rad51"

FT misc_binding 311..328

FT /*tag= d

FT /bound_moiety= "AS3"

FT misc_binding 425..438

FT /*tag= e

FT /bound_moiety= "AS1"

FT misc_binding 635..649

FT /*tag= f

FT /bound_moiety= "AS2"

FT misc_binding 1524..1545

FT /*tag= g

FT /bound_moiety= "AS6"

FT misc_binding 1881..1902

FT /*tag= h

FT /bound_moiety= "AS7"

FT misc_binding 1911..1933

FT /*tag= i

FT /bound_moiety= "AS8"

FT misc_binding 2038..2060

FT /*tag= j

FT /bound_moiety= "AS9"

XX WO200047231-A2.

XX 17-AUG-2000.

XX 03-FEB-2000; 2000WO-US002881.

XX 10-FEB-1999; 99US-0119578P.

XX 06-DEC-1999; 99US-00454495.

XX (PANG-) PANGENE CORP.

XX Reddy G;

XX WPI; 2000-506091/45.

XX Inhibiting cell proliferation useful for cancer therapy, comprises
PT administering Rad51 inhibitor in vivo.

XX Disclosure; Fig 9b-9a; 42pp; English.

CC This sequence is the human Rad51 mRNA sequence. Antisense inhibitors of
 CC this sequence can be used in a method for inhibiting cell proliferation.
 CC They can also be used in methods for inducing sensitivity to radiation
 CC and DNA damaging chemotherapeutics in an individual and in a method for
 CC prolonging survival in an individual with cancer. The methods and
 CC antisense molecules are useful for inhibiting cell proliferation,
 CC especially cancerous cell proliferation, for inducing sensitivity to
 CC radiation and DNA damaging chemotherapeutics in individuals and for
 CC prolonging survival in an individual with cancer. Kits for carrying out
 CC the methods may be used to diagnose and/or treat cancer and for
 CC adjunctive therapy. Note: In the specification, the 3' end of this
 CC sequence is shown in figure 9a, while the 5' end of this sequence is
 CC given in figure 9b
 XX
 SQ Sequence 2229 BP; 593 A; 472 C; 602 G; 562 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 3; Length 2229;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACCTAATTC 15
 Db 439 GGCTTCACCTAATTC 425

RESULT 11

RAD51209/C

ID AAS01209 standard; cDNA; 2229 BP.

XX AAS01209;

XX 04-JUL-2001 (first entry)

XX Human RAD51 cDNA sequence.

XX Human; Rad51; antisense; drug screening; cancer; autoimmune disease;
 XX arthritis; graft rejection; inflammatory bowel disease; surgery;
 KW angioplasty; ss.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 primer_bind complement(403..425)

FT /tag= a
 FT /note= "Binds antisense oligonucleotide AS6"
 FT complement(761..782)

FT /tag= b
 FT /note= "Binds antisense oligonucleotide AS7"
 FT complement(791..813)

FT /tag= c
 FT /note= "Binds antisense oligonucleotide AS8"
 FT complement(918..940)

FT /tag= d
 FT /note= "Binds antisense oligonucleotide AS9"
 FT complement(1110..1115)

FT /tag= e
 FT /note= "Binds antisense oligonucleotide AS4"
 FT complement(1258..1267)

FT /tag= f
 FT /note= "Binds antisense oligonucleotide AS5"
 FT complement(1413..1424)

FT /tag= g
 FT /note= "Binds antisense oligonucleotide AS3"
 FT complement(1455..1468)

FT /tag= h
 FT /note= "Binds antisense oligonucleotide AS1"
 FT complement(1745..1759)

FT /tag= i
 FT /note= "Binds antisense oligonucleotide AS2"
 FT complement(1745..1759)

WO200119397-A1.

22-MAR-2001.

XX 18-SEP-2000; 2000WO-US025838.

XX 17-SEP-1999; 99US-0154616P.

XX 06-DEC-1999; 99US-00455300.

XX (PANG-) PANGENE CORP.

XX Reddy G;

XX WPI; 2001-244704/25.

XX Inhibiting cell proliferation for treating arthritis, graft rejection,
 XX inflammatory bowel disease, cancer, proliferation induced after medical
 XX procedure, involves administering Rad51 antibody or its fragment to cell.

XX Disclosure; Fig 15; 102pp; English.

XX The sequence represents the coding sequence of human Rad51. Rad51 protein
 XX is defective in repair of damaged DNA, genetic recombination and the
 XX recombinational repair of DNA lesions, and plays a central role in
 XX cancer. The sequence was used to design antisense oligonucleotides which
 XX were used to study down-regulation of Rad51 protein in human brain,
 XX breast and prostate cells. Inhibiting cell proliferation involves
 XX administering to a cell a Rad51 antibody or its fragment. The Rad51
 XX antibody or its fragment is useful for inhibiting cell proliferation, for
 XX treating disease states such as cancer, autoimmune disease, arthritis,
 XX graft rejection, inflammatory bowel disease, proliferation induced after
 XX medical procedures such as surgery, angioplasty etc. in humans and
 XX animals

XX Sequence 2229 BP; 593 A; 472 C; 602 G; 562 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 15; DB 4; Length 2229;

XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACCTAATTC 15

Db 1548 GGCTTCACCTAATTC 1534

RESULT 12

ADA02555/c

ID ADA02555 standard; DNA; 21565 BP.

XX ADA02555;

XX 06-NOV-2003 (first entry)

XX Mouse Ly6e carcinoma associated gene, SEQ ID NO:1073.

XX Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;
 XX prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
 XX gene; ds.

XX Mus sp.

XX WO2003057146-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041414.

XX 26-DEC-2001; 2001US-00035832.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW;

XX WPI; 2003-587068/55.

XX New recombinant nucleic acid encoding carcinoma associated protein,

XX

PT useful for preparing compositions for treating carcinomas.
 PS Claim 1; SEQ ID NO 1073; 245pp; English.
 XX
 CC The invention relates to recombinant carcinoma associated (CA) nucleic
 CC acid sequences from mouse and human (ADA01482-ADA03094), and to
 CC recombinant carcinoma associated proteins (CAP) encoded by them. The
 CC invention also encompasses expression vectors and host cells comprising a
 CC CA nucleic acid, a polypeptide (especially an antibody) that specifically
 CC binds to the protein, and a biochip comprising CA nucleic acid or
 CC fragments thereof. The sequences of the invention were identified using
 CC oncogenic retroviruses, which insert into the genome of the host organism
 CC at random. Many of these do not carry transduced host oncogenes or
 CC pathogenic trans-acting viral genes, meaning that cancer incidence is a
 CC direct consequence of the effects of proviral integration into host
 CC protooncogenes. The CA nucleic acid sequences can be used to diagnose
 CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
 CC leukaemia) or a propensity to carcinoma by determination of the sequence
 CC of a CA gene, or by determination of CA gene expression in particular
 CC tissues. CA nucleic acids, proteins and antibodies are also useful as
 CC therapeutic agents and in screening and evaluating drug candidates. The
 CC present sequence represents a specifically claimed murine CA nucleic acid
 CC sequence of the invention. Note: The complete sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 21565 BP; 5397 A; 5271 G; 5466 G; 5371 T; 0 U; 60 Other;

Query Match 100.0%; Score 15; DB 8; Length 21565;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

DB 8820 GGCTTCACTAATTC 8806

RESULT 13

ADB72293/c
 ID ADB72293 standard; DNA; 21565 BP.

AC ADB72293;

DT 04-DEC-2003 (first entry)

DE Mouse Ly6e gene.

XX mouse; ds; cytostatic; Gene therapy; vaccine; carcinoma; lymphomas;
 KW cancer; neoplasm; adenocarcinoma; sarcoma; gene.

XX Mus sp.

FN WO2003008583-A2.

PD 30-JAN-2003.

PF 26-DEC-2001; 2001WO-US051291.

XX 02-MAR-2001; 2001US-0079586.

FR 23-OCT-2001; 2001US-00004113.

FR 08-NOV-2001; 2001US-00052482.

FR 30-NOV-2001; 2001US-00997722.

FR 20-DEC-2001; 2001US-00034650.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW, Engelhard EK;

XX WPI; 2003-239337/23.

XX New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
 PT cancers, neoplasm, adenocarcinoma, or sarcomas.

XX PS Claim 1; SEQ ID NO 121; 2304pp; English.

XX CC The invention relates to a novel recombinant nucleic acid comprising a
 CC nucleotide sequence selected from any of the 660 sequences fully defined
 CC in the specification. A polynucleotide of the invention has cytostatic
 CC activity, and may have a use in gene therapy, or in a vaccine. The
 CC recombinant nucleic acids and polypeptides are useful for treating
 CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
 CC sarcomas. The present sequence represents a mouse gene of the invention.

XX SQ Sequence 21565 BP; 5397 A; 5271 C; 5466 G; 5371 T; 0 U; 60 Other;

Query Match 100.0%; Score 15; DB 9; Length 21565;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

DB 8820 GGCTTCACTAATTC 8806

RESULT 14

AAH41223

ID AAH41223 standard; DNA; 349980 BP.

XX AC AAH41223;

DT 29-OCT-2001 (first entry)

XX Pyrococcus abyssi genomic fragment #2.

XX Hyperthermophilic archaeon; hyperthermophilic protein; ds.

XX Pyrococcus abyssi.

XX Key Location/Qualifiers

FT misc_feature 1..49980

FT /tag= a

FT /note= "This sequence overlaps with the 3' end of

FT AAF86431"

FT misc_feature 300001..349980

FT /tag= b

FT /note= "This sequence overlaps with the 5' end of

FT AAF41224"

XX PR2792651-A1.

XX 27-OCT-2000.

XX 21-APR-1999; 99FR-00005034.

XX 21-APR-1999; 99FR-00005034.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX (IFRE-) IFREMER INST FR RECH EXPL MER.

XX Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;

XX Querellou J, Weissenbach J, Saurin W, Heilig R;

XX WPI; 2001-126236/14.

XX New nucleotide sequences isolated from Pyrococcus abyssi encode proteins
 XX useful in industry.

XX Claim 1; Page 265-361; 1657pp; French.

XX The present invention relates to the genomic sequence of Pyrococcus

XX abyssi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a

XX hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal

XX vents. The present sequence is a fragment of the genomic sequence of P.

XX abyssi. The 5' end of this sequence overlaps with the 3' end of AAF86431

XX and the 3' end of this sequence overlaps with the 5' end of AAH41224. The

CC proteins of the present invention have various potential industrial uses,
CC since the proteins are stable at very high temperatures, some up to 110
CC degrees centigrade. Note: This patent is in the same patent family as
CC WO200605062, which contains additional sequences as shown in AAB99132-
CC AAB99143, AAB75903-AAH75920 and AAG66436
XX
SQ Sequence 349980 BP; 92953 A; 77841 C; 81831 G; 97355 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 5; Length 349980;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

Qy 1 GGCTTCACTAATTC 15
Db 281481 GGCTTCACTAATTC 281495

RESULT 15
ABZ23353/c
ID ABZ23353 standard; DNA; 18 BP.

XX ABZ23353;

XX 07-APR-2003 (first entry)

Forward PCR primer used to amplify porcine RAD51 cDNA.

Antigenic determinant; immunotolerance; cell therapy; liver condition;
xenotransplantation; heart condition; pancreatic condition;
kidney condition; lung condition; RAD51; PCR; primer; ss.

XX Sus sp.

XX WO200292791-A1.

XX 21-NOV-2002.

XX 14-MAY-2002; 2002WO-US015307.

XX 14-MAY-2001; 2001US-0291394P.

XX 13-AUG-2001; 2001US-0312125P.

XX 21-MAR-2002; 2002US-0367090P.

XX (STEL-) STELL.

XX Liljedahl M, Marcantonio D, Aspland SE;

XX WPI; 2003-120679/11.

XX Novel genetically engineered cell in which a gene comprising an antigenic
XX determinant recognized by a recipient organism has been disrupted, useful
XX in cell therapy or xenotransplantation.

XX Example 9; Page 44; 97pp; English.

XX The specification describes genetically engineered cell in which at least
XX one gene encoding a polypeptide comprising an antigenic determinant which
XX is recognized by a desired recipient organism or at least one gene which
XX encodes a protein associated with the synthesis of a molecule comprising
XX the antigenic determinant has been disrupted. The genetically engineered
XX cell has a reduced level of immunogenicity in the recipient and can be
XX safely transplanted across species. It reduces the amount of medication
XX required to induce a state of immunotolerance in the host. The genetically
XX engineered cells of the invention are useful in cell therapy, or to
XX produce tissues or organs for use in xenotransplantation. They are useful
XX for treating heart conditions (e.g., valvular heart disease), liver
XX conditions (e.g., liver cirrhosis), pancreatic conditions (e.g.,
XX diabetes), kidney conditions (e.g., primary glomerulonephritis), lung
XX conditions (e.g., cystic fibrosis), Alzheimer's disease, stroke,
XX Parkinson's disease, cataracts and Creutzfeldt-Jacob disease. PCR primers
XX ABZ23353-54 were used to amplify a 407 bp fragment of porcine RAD51 cDNA.
XX The amplified fragment is used as a probe to identify homologous sequence
XX to enhance homologous recombination in the course of the invention

XX
SQ Sequence 18 BP; 8 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 93.3%; Score 14; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCTTCACTAATTC 14
Db 14 GGCTTCACTAATTC 1

Search completed: March 21, 2004, 21:10:35
Job time : 288 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 19:46:36 ; Search time 1531.5 Seconds
(without alignments)
424.516 Million cell updates/sec

Title: US-09-260-624a-1
Perfect score: 15
Sequence: 1 ggttcactaattcc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: gb.in.*
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- 6: gb.ph.*
- 7: gb.pl.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.sts.*
- 11: gb.un.*
- 12: gb.vi.*
- 13: gb.vt.*
- 14: gb.vt.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
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- 19: em.mu.*
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- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	15	100.0	15	6	BD271099	Novel ant
2	15	100.0	15	6	AR343098	Sequence
3	15	100.0	15	6	AX099904	Sequence
C 4	15	100.0	15	6	AX099907	Sequence
5	15	100.0	15	6	AX492789	Sequence
6	15	100.0	20	6	AX084202	Sequence
C 7	15	100.0	425	9	AY425955	Sequence
C 8	15	100.0	550	11	G80435	Sequence
C 9	15	100.0	1020	10	CGRAD51	Sequence
C 10	15	100.0	1389	8	AB080262	Oryza sat
C 11	15	100.0	1408	6	E09402	Mouse mrna
C 12	15	100.0	1408	10	MUSRAD51A	Mouse mrna
C 13	15	100.0	1417	9	BC001459	Homo sapi
C 14	15	100.0	1645	6	AX771463	Sequence
C 15	15	100.0	1645	9	HUMRAD51B	Human mrna
C 16	15	100.0	1682	6	E09404	Human mrna
C 17	15	100.0	1745	10	MUSRAD51	Mouse mrna
C 18	15	100.0	1755	6	E07535	Clone pMR51
C 19	15	100.0	2121	10	BC027384	Mouse muscu
C 20	15	100.0	2229	6	BD271098	Novel ant
C 21	15	100.0	2229	6	AR343097	Sequence
C 22	15	100.0	2229	6	AX099913	Sequence
C 23	15	100.0	2229	9	HUMRAD51	Human mrna
C 24	15	100.0	2363	9	AF233739S3	Homo sapi
C 25	15	100.0	3006	8	AB080361	Oryza sat
C 26	15	100.0	4823	10	CRUKJCG1	Cricetulus
C 27	15	100.0	5799	10	MM047737	Mouse muscu
C 28	15	100.0	7606	9	HS51RAD1	Homo sapi
C 29	15	100.0	8153	9	AF203691	Homo sapi
C 30	15	100.0	21565	6	AX695446	Sequence
C 31	15	100.0	26083	3	U53339	Caenorhabdi
C 32	15	100.0	39521	9	AY196785	Homo sapi
C 33	15	100.0	59231	9	AL135937	Human DNA
C 34	15	100.0	61332	2	AC084029	Homo sapi
C 35	15	100.0	61332	2	AC084029	Homo sapi
C 36	15	100.0	143104	9	AL606503	Human DNA
C 37	15	100.0	147665	9	AL138691	Human DNA
C 38	15	100.0	151186	2	AC068750	Homo sapi
C 39	15	100.0	153680	9	AC093003	Homo sapi
C 40	15	100.0	154494	2	AC120885	Oryza sat
C 41	15	100.0	154494	2	AC120885	Oryza sat
C 42	15	100.0	158510	9	AC079090	Homo sapi
C 43	15	100.0	166093	2	AC015462	Homo sapi
C 44	15	100.0	167857	9	AL138778	Human DNA
C 45	15	100.0	169723	2	AC127987	Rattus no

ALIGNMENTS

RESULT 1	BD271099	15 bp	DNA	linear	PAT 07-AUG-2003
LOCUS	BD271099	Novel antisense inhibition of Rad51.			
DEFINITION	BD271099	Novel antisense inhibition of Rad51.			
ACCESSION	BD271099	Novel antisense inhibition of Rad51.			
VERSION	BD271099.1	GI:33080857			
KEYWORDS	JP 2002536420-A/2.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 15)				
AUTHORS	Zeng,H., Reddy,G., Valleria,A. and Zarling,D.A.				
TITLE	Novel antisense inhibition of Rad51				
JOURNAL	Patent: JP 2002536420-A 2 29-OCT-2002;				
	PANGENE CORP				

COMMENT OS Artificial Sequence
PN JP 2002536420-A/2
PD 29-OCT-2002
PF 03-FEB-2000 JP 2000598182
PR 10-FEB-1999 US 60/119578,06-DEC-1999 US 09/454495 PI
HONG ZENG,GURUCHARAN REDDY,ANNE VALLERGA,DAVID A ZARLING PC
A61K45/00,A61K31/7088,A61K48/00,A61P1/00,A61P19/02,A61P29/00, PC
A61P35/00,
PC A61P37/06,G01N33/50
CC Description of Artificial Sequence: synthetic FH Key
Location/Qualifiers
FT source 1..15
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
Db 1 GGCTTCACTAATTC 15
RESULT 2
AR343098
LOCUS AR343098 15 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 2 from patent US 6576759.
ACCESSION AR343098
VERSION AR343098.1 GI:33738509
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Zeng,H., Reddy,G., VallerGA,A. and Zarling,D.A.
TITLE Antisense inhibition of RAD51
JOURNAL Patent: US 6576759-A 2 10-JUN-2003;
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Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
Db 1 GGCTTCACTAATTC 15
RESULT 3
AX099904
LOCUS AX099904 15 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 7 from Patent WO0119397.
ACCESSION AX099904
VERSION AX099904.1 GI:13538930
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Reddy,G.
TITLE Methods and compositions utilizing rad51
JOURNAL Patent: WO 0119397-A 7 22-MAR-2001;
Pangene Corporation (US)

FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
Db 1 GGCTTCACTAATTC 15
RESULT 4
AX099907/c
LOCUS AX099907 15 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 10 from Patent WO0119397.
ACCESSION AX099907
VERSION AX099907.1 GI:13538933
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Reddy,G.
TITLE Methods and compositions utilizing rad51
JOURNAL Patent: WO 0119397-A 10 22-MAR-2001;
Pangene Corporation (US)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide"
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Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
Db 15 GGCTTCACTAATTC 1
RESULT 5
AX492789
LOCUS AX492789 15 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1 from Patent WO02058738.
ACCESSION AX492789
VERSION AX492789.1 GI:23338472
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Zarling,D.A. and Reddy,G.
TITLE Use of rad51 inhibitors for p53 gene therapy
JOURNAL Patent: WO 02058738-A 1 01-AUG-2002;
PANGENE CORP (US)
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTTCACCTAATCC 15
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RESULT 6
AX084202
LOCUS AX084202 20 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 18 from Patent WO0111369.
ACCESSION AX084202
VERSION AX084202.1 GI:13185709
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Sturzebecher, H.W. and Reddy, G.
TITLE Cancer treatments and diagnostics utilizing rad51 related molecules
and methods
JOURNAL Patent: WO 0111369-A 18 15-FEB-2001;
Pangene Corporation (US)
FEATURES
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/organism="synthetic construct"
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ORIGIN
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTTCACCTAATCC 15
Db 2 GGCTTCACCTAATCC 16

RESULT 7
AX425955/c
LOCUS AX425955 425 bp mRNA linear PRI 03-NOV-2003
DEFINITION Homo sapiens Rad51 mRNA, partial cds, alternatively spliced.
ACCESSION AY425955
VERSION AY425955.1 GI:38017104
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venables, J.P.
TITLE Alternative splicing in the testes
JOURNAL Unpublished
REFERENCE 2
AUTHORS Venables, J.P.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2003) Institute of Human Genetics, Newcastle
University, International Centre for Life, Central Parkway,
Newcastle upon Tyne, England NE1 3BZ, UK
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/codon_start=3
/product="Rad51"

CDS
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Query Match 100.0%; Score 15; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTTCACCTAATCC 15
Db 53 GGCTTCACCTAATCC 39

RESULT 8
G80435
LOCUS G80435 550 bp DNA linear STS 06-SEP-2002
DEFINITION S210P6047FH1.T0 BALB/cByJ Mus musculus STS genomic, sequence tagged
site.
ACCESSION G80435
VERSION G80435.1 GI:22731191
KEYWORDS STS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Wade, C.
TITLE Polymorphism Structure in the Mouse
JOURNAL Unpublished (2002)
COMMENT
Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 550
Protocol:
WGS-discovery: Paired-end low-coverage whole genome shotgun reads
were generated from 129S1/SvimJ, C3H/HeJ, and BALB/cByJ. The WGS
reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP
detection was carried out by SSAHA-SNP. 225,000 reads were
annotated
as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J
and the strain from which the particular read came. The validation
rate for these SNPs was estimated at approximately 98%.
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Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTTCACCTAATCC 15
Db 465 GGCTTCACCTAATCC 451

RESULT 9
CGRAD51/c

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LOCUS CGRAD51 1020 bp mRNA linear ROD 05-JUN-1998
DEFINITION C-griseus mRNA for RAD51 protein.
ACCESSION Y08202
VERSION Y08202.1 GI:1552257
KEYWORDS DNA repair; RAD51 gene.
SOURCE Cricetulus griseus (Chinese hamster)
ORGANISM Cricetulus griseus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Cricetulus.
REFERENCE 1. Vispe,S., Cazaux,C., Lesca,C. and Defais,M.
Overexpression of Rad51 protein stimulates homologous recombination
and increases resistance of mammalian cells to ionizing radiation
Nucleic Acids Res. 26 (12), 2859-2864 (1998)
JOURNAL 98278898
MEDLINE 9611228
REFERENCE 2. (bases 1 to 1020)
AUTHORS Vispe,S.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-1996) S. Vispe, CNRS, IPBS, 205 route de
Narbonne, F- 31400 Toulouse, FRANCE
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ORIGIN
Query Match 100.0%; Score 15; DB 10; Length 1020;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCTTCACCTAATTC 15
Db 207 GGCTTCACCTAATTC 193
RESULT 10
LOCUS AB080262/c
DEFINITION Oryza sativa (japonica cultivar-group) OsRad51A1 mRNA for Rad51,
complete cds.
ACCESSION AB080262
VERSION AB080262.1 GI:18874070
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1. Shimizu,T., Mimida,N., Nakamura,S., Kawasaki,S., Nakashima,M.,
Oshikabe,K., Toki,S. and Ichikawa,H.
Homologous recombination related genes, Rad51 in rice
Published Only in Database (2002)
JOURNAL 2 (bases 1 to 1389)
AUTHORS Shimizu,T., Mimida,N., Nakamura,S., Kawasaki,S., Nakashima,M.,
Oshikabe,K., Toki,S. and Ichikawa,H.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2002) Naozumi Mimida, National Institute of
Agrobiological Sciences, Department of Plant Biotechnology,
Kannondai-2-1-2, Tsuba, Ibaraki 305-8602, Japan
IS-mail: mmd@affrc.go.jp, Tel: 81-298-38-7442, Fax: 81-298-38-7073)
FEATURES
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AMFAGPQIKPIGNNIMAHASTRLALRRGRGERICKYVSSPCIAEAARFQIASEGV
ADVKD"

LOCUS E09402 1408 bp RNA linear PAT 29-SEP-1997
DEFINITION RAD51 structural gene.
ACCESSION E09402
VERSION E09402.1 GI:22026029
KEYWORDS JP 1995143890-A/1.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1. (bases 1 to 1408)
AUTHORS Shinohara,A., Namajio,N., Ogawa,H. and Ogawa,T.
TITLE RAD51 STRUCTURE GENE
JOURNAL Patent: JP 1995143890-A 1 06-JUN-1995;
TOYOBO CO LTD
COMMENT OS Mus musculus (mouse)
PN JP 1995143890-A/1
PD 06-JUN-1995
PF 28-MAY-1993 JP 1993127594
PI SHINOHARA AKIRA, NAMAJIO NORIKO, OGAWA HIDEYUKI, OGAWA TOMOKO
PC C12N15/12, C12N1/19, C12N5/10, C12P21/02, (C12N1/19, C12R1/865), PC
(C12P21/02,
PC C12R1/865), (C12P21/02, C12R1/19), (C12P21/02, C12R1/91); CC
strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC Feature is identified by experimental;
FH Key Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACCTAATTC 15
Db 395 GGCTTCACCTAATTC 381

RESULT 12
MUSRAD51A/c
LOCUS
DEFINITION Mouse mRNA for RecA-like protein MmRad51, complete cds.
ACCESSION D13803
VERSION D13803.1 GI:303702
KEYWORDS ATPase; DNA repair; MmRad51; RecA-like protein; meiosis;
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1408)
AUTHORS Shinohara,A., Ogawa,H., Matsuda,Y., Ushio,N., Ikeo,K. and Ogawa,T.
TITLE Cloning of human, mouse and fission yeast recombination genes
homologous to RAD51 and recA
JOURNAL Nat. Genet. 4 (3), 239-243 (1993)
MEDLINE 93364417
PUBMED 8358431
REFERENCE 2 (bases 1 to 1408)
AUTHORS Shinohara,A.
DIRECT SUBMISSION
TITLE Submitted (02-DEC-1992) Akira Shinohara, Faculty of Science, Osaka
University, Department of Biology, Toyonaka, Osaka 560, Japan
(JE-mail:c62528@center.osaka-u.ac.jp, Tel:06-844-1151(ex.4305),
Fax:06-841-2449)
COMMENT Submitted (02-DEC-1992) to DDBJ by:
Akira Shinohara
Department of Biology
Faculty of Science
Osaka University
1-1 Machikaneyama
Toyonaka, Osaka 560
Japan
Phone: 06-844-1151 x4305
Email: c62528@center.osaka-u.ac.jp
Fax: 06-841-2449.

FEATURES
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Query Match 100.0%; Score 15; DB 10; Length 1408;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACCTAATTC 15
Db 395 GGCTTCACCTAATTC 381

RESULT 13
BC001459/c
LOCUS
DEFINITION Homo sapiens RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae),
transcript variant 2, mRNA (cDNA clone MGC:2244 IMAGE:3139011),
complete cds.
ACCESSION BC001459
VERSION BC001459.2 GI:33876241
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1417)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,J., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Shat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heide,P.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullen,J.S., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,D.J., Hulyk,S.W.,
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Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywicki,M.I., Skalski,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1417)
AUTHORS Strausberg,R.
DIRECT SUBMISSION
TITLE Submitted (12-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT On Aug 19, 2003 this sequence version replaced gi:13655202.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov

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ORIGIN
Query Match      100.0%; Score 15; DB 9; Length 1417;
Best Local Similarity 100.0%; Pred. No. Se+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
AX771463/c
LOCUS
DEFINITION
Sequence 176 from Parent WO03004646.
AX771463
ACCESSION
AX771463.1 GI:32438939
VERSION
KEYWORDS

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Best Local Similarity 100.0%; Freq. No. 5e-02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 1537.5 secs